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OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 03:22:05 ; Search time 2219 Seconds
(without alignments)
18906.432 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

Sequence: 1 gccagcccccagattgggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 23Sep04:.*
1: geneseqn1980s:.*
2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001as:.*
5: geneseqn2001bs:.*
6: geneseqn2002as:.*
7: geneseqn2002bs:.*
8: geneseqn2003as:.*
9: geneseqn2003bs:.*
10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	7992	100.0	7992	6	AAL47276 Hepatitis
2	7992	100.0	10690	6	ABK91412 Hepatitis
3	7992	100.0	10690	9	ACA61697 Hepatitis
4	7992	100.0	10690	10	ADC83762 Hepatitis
5	7990.4	100.0	7992	6	AAL47281 Hepatitis
6	7990.4	100.0	10690	6	ABK91428 Hepatitis
7	7990.4	100.0	10690	6	ABK91435 Hepatitis
8	7990.4	100.0	10690	6	ABK91243 Hepatitis
9	7990.4	100.0	10690	6	ABK91434 Hepatitis
10	7990.4	100.0	11313	12	ADP86264 Hepatitis
11	7989	100.0	7989	3	AAA98968 Hepatitis
12	7989	100.0	7989	12	ADJ57845 HCV repli
13	7988.8	100.0	10690	6	ABK91440 Hepatitis
14	7988.8	100.0	11313	12	ADP86271 Hepatitis
15	7987.4	99.9	7989	6	AAD25322 Hepatitis
16	7987.2	99.9	7992	6	AAL47280 Hepatitis
17	7987.2	99.9	7992	6	AAL47277 Hepatitis
18	7987.2	99.9	11313	12	ADP86265 Hepatitis
19	7985.8	99.9	7989	6	AAD25326 Hepatitis
20	7985.6	99.9	11313	12	ADP86272 Hepatitis
21	7984	99.9	10690	6	ABK91242 Hepatitis

22	7982.6	99.9	7989	6	AAD25325 Hepatitis
23	7982.6	99.9	7989	10	ADD93734 Hepatitis
24	7982.4	99.9	11313	12	ADP86275 Hepatitis
25	7981	99.9	10691	6	ABK91423 Hepatitis
26	7980.8	99.9	11313	12	ADP86273 Hepatitis
27	7979.2	99.8	11313	12	ADP86266 Hepatitis
28	7979	99.8	10693	6	ABK91438 Hepatitis
29	7977.6	99.8	11313	12	ADP86268 Hepatitis
30	7977.4	99.8	10693	6	ABK91443 Hepatitis
31	7976.2	99.8	10691	6	ABK91439 Hepatitis
32	7975	99.8	7987	6	AAD25321 Hepatitis
33	7974.4	99.8	11313	12	ADP86267 Hepatitis
34	7973.6	99.8	7991	6	AAL47279 Hepatitis
35	7973.4	99.8	7987	6	AAD25329 Hepatitis
36	7971.8	99.7	7987	6	AAD25324 Hepatitis
37	7967	99.7	8001	3	AAA98967 Hepatitis
38	7966.2	99.7	7995	6	AAL47278 Hepatitis
39	7958.4	99.6	11313	12	ADP86270 Hepatitis
40	7955.2	99.5	11313	12	ADP86269 Hepatitis
41	7777.8	97.3	7989	10	ADD93733 Hepatitis
42	7714.4	96.5	11184	12	ADP86274 Hepatitis
43	7706.4	96.4	11184	12	ADP86276 Hepatitis
44	7701.6	96.4	11184	12	ADP86277 Hepatitis
45	7695.4	96.3	7848	6	AAD25323 Hepatitis

ALIGNMENTS

RESULT 1

AAL47276

ID AAL47276 standard; DNA; 7992 BP.

XX

AC AAL47276;

XX

DT 30-AUG-2002 (first entry)

XX

DE Hepatitis C virus sub-genomic replicon clone I377-NS3-3'UTR.

XX

KW Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis; virucide; hepatotropic; gene therapy; anti-viral; gene; ds.

XX

OS Hepatitis C virus.

XX

FR Key Location/Qualifiers

FT CDS

FT 342..1181

FT /*tag= a

FT /*product= "core-neo fusion protein"

FT 1801..7758

FT /*tag= b

FT /*product= "NS3 proteinase/helicase"

XX

PN WO200238793-A2.

XX

PD 16-MAY-2002.

XX

PF 02-NOV-2001; 2001WO-US046350.

XX

PR 07-NOV-2000; 2000US-0245866P.

XX

PA (ANAD-) ANADYS PHARM INC.

XX

PI Bichko V;

XX

DR WPI; 2002-490082/52.

DR

P-PSDB; AAO18000, AAO18001.

XX

PT Novel nucleic acid encoding replication competent recombinant hepatitis C virus genome useful for screening anti-hepatitis C virus therapeutics and for vaccine development.

XX

PS Claim 6; Page 43-47; 85pp; English.

XX

The present invention provides protein and coding sequences from Hepatitis C virus (HCV), comprising all or part of the HCV genome and able to replicate efficiently when transfected into a susceptible cell line without reducing the growth rate of the cell line by more than 10 fold. The sequences are useful for screening for anti-HCV therapeutics, for detecting antibodies to HCV in a biological sample such as blood, serum, plasma, blood cells, lymphocytes, or liver cells from a subject, for deriving authentic HCV components such as replication-complement non-infectious, replication-defective infection-component, and replication-defective non-infectious HCV, in gene therapy or gene vaccination targeted to hepatic tissue for treating an animal infected or susceptible to HCV infection and for studying HCV infection and propagation. The present sequence is a clone of a fragment of the HCV genome which encodes the core-neo and NS3 proteinase/helicase proteins

Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 U; 0 Other;

Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 U; 0 Other;

Query Match	100.0%;	Score 7992;	DB 6;	Length 7992;
Best local Similarity	100.0%;	Pred. No. 0;		
Matches 7992;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY 61	TCTTACGCGAGAAAGCGTCTAGCCATGGCGTGTAGTATGATGTGCTGCACGCTCCAGGAC	120		
DB 61	TCTTACGCGAGAAAGCGTCTAGCCATGGCGTGTAGTATGATGTGCTGCACGCTCCAGGAC	120		
QY 121	CCCCCTCCCCGGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATGGCCAG	180		
DB 121	CCCCCTCCCCGGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATGGCCAG	180		
QY 181	GACGACCGGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGCGTGCCTCC	240		
DB 181	GACGACCGGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGCGTGCCTCC	240		
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DB 241	GCGAGACTGTAGCCGAGTAGTGTGGTTCGCGAAGGSCCTTGTGTACTCCCTGATAGG	300		
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DB 301	GTGCTTGGAGTGCCTCCCGGAGGTCCTGTAGACCGTGACCATGAGCAGAACTCTAAAC	360		
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DB 361	CTCAAAGAAAAACCAAGGGCGGCGCATGATTGAACAAGATGGATTGCACGAGTCTC	420		
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DB 421	CGGCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCACAAAGACAATCGGCTGT	480		
QY 481	CTGATGCCCGCGTGTTCGGCTGTACGCGCAGGGCGCCGGTCTTTTGTTCAGACCG	540		
DB 481	CTGATGCCCGCGTGTTCGGCTGTACGCGCAGGGCGCCGGTCTTTTGTTCAGACCG	540		
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DB 541	ACTGTCCGCTGCCCTGAATGAAGTCCAGACGAGGACGCGGCTATCGTGCCTGGCCA	600		
QY 601	CGACGGGCGTTCCTTTCGCGAGCTGTGCTCGACGCTTCTCACTGAAGCGGGAAGGACTGCG	660		
DB 601	CGACGGGCGTTCCTTTCGCGAGCTGTGCTCGACGCTTCTCACTGAAGCGGGAAGGACTGCG	660		
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DB 661	TGCTATTGGCGAAGTGCCTGGGGGAGGATCTCTGTTCATCTCACTTGTCTCTGGCCGAGA	720		
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DB 721	AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCGGGTCACTGCG	780		

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[illegible]

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XX	PD	16-JAN-2002; 2002WO-EP000526.	
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XX	PR	(RICE-) IST RICERHE BIOL MOLECOLARE ANGELETII.	
XX	PA	De Francesco R, Migliaccio G, Paonessa G;	
XX	PI	WPT; 2002-599793/64..	
DR	XX	New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region, useful in studying HCV replication and expression. Claim 1; Fig 1; 69pp; English.	
CC	XX	The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell/human hepatoma cell comprising the altered nucleic acids ; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is the HCV based vector pHCYNeo.17, used as a basis for the adaptive mutations of the invention	
CC	XX	Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;	
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QY	121	CCCCTCCCGGAGAACCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180 	
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QY 2701 ATCTTGGGCATCGGCACAGTCTGACCAAGCGAGAGCGCTGAGCGCACTCGTCTGTG 2760
DB 2701 ATCTTGGGCATCGGCACAGTCTGACCAAGCGAGAGCGCTGAGCGCACTCGTCTGTG 2760
QY 2761 CTGCGCACCGCTACGCTCCGGGATCGGTCACTGCGCACATCCAAACATCGAGAGGTG 2820
DB 2761 CTGCGCACCGCTACGCTCCGGGATCGGTCACTGCGCACATCCAAACATCGAGAGGTG 2820
QY 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGSCAAAGCCATCCCATCGAGACCACT 2880
DB 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGSCAAAGCCATCCCATCGAGACCACT 2880
QY 2881 AAGGGGGGAGGACCTCATTTCTGCGCATTCAGAGAAATGTGATGAGCTGCGCGG 2940
DB 2881 AAGGGGGGAGGACCTCATTTCTGCGCATTCAGAGAAATGTGATGAGCTGCGCGG 2940
QY 2941 AAGTGTCCGCTCGGACTCAATGCTGATGATATTAACCGGGGCTTGTATGATCCGTC 3000
DB 2941 AAGTGTCCGCTCGGACTCAATGCTGATGATATTAACCGGGGCTTGTATGATCCGTC 3000
QY 3001 ATACCACTAGCGAGAGCTCATTTGTGTAGCAACGAGACGCTCTAATGACGGGCTTTACC 3060
DB 3001 ATACCACTAGCGAGAGCTCATTTGTGTAGCAACGAGACGCTCTAATGACGGGCTTTACC 3060
QY 3061 GGCATTTCCGACTCAGTGTGACTGCAATATCATGTGTACCCAGACAGTCTGAGC 3120
DB 3061 GGCATTTCCGACTCAGTGTGACTGCAATATCATGTGTACCCAGACAGTCTGAGC 3120
QY 3121 CTGACCCGACCTTCACTTGGACAGCAGCCTGCGCAACAGCGGGTGTACGCTCG 3180
DB 3121 CTGACCCGACCTTCACTTGGACAGCAGCCTGCGCAACAGCGGGTGTACGCTCG 3180
QY 3181 CAGCGGAGGACGAGCTGTTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240
DB 3181 CAGCGGAGGACGAGCTGTTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240
QY 3241 GAACGGGCTTCCGGCATGTTTCGATTCCTGCTGCGAGTGTATGACGGGGCTGT 3300
DB 3241 GAACGGGCTTCCGGCATGTTTCGATTCCTGCTGCGAGTGTATGACGGGGCTGT 3300
QY 3301 GCTTGTGACGAGCTACGCGCCGCGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA 3360
DB 3301 GCTTGTGACGAGCTACGCGCCGCGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA 3360
QY 3361 CAGGGTGTGCGCTGTGCGAGGACCATCTGAGTTCCTGGAGAGCGCTTTTACAGGCTC 3420
DB 3361 CAGGGTGTGCGCTGTGCGAGGACCATCTGAGTTCCTGGAGAGCGCTTTTACAGGCTC 3420
QY 3421 ACCACATAGACCCCATTTCTTGTCCGACACTAAGCAGCAGGACACATTTCCCTAC 3480

Db	3421	ACCCATAGACGCCCATTTCTTCCAGACTAAGCAGGACAGACAACATTCCTCCCTAC	3480	QY	4561	CAGATCTCTCTAGTCTTACCATCACTAGCTGCTGAAGAGGCTTACCAGTGGATCAAC	4620
QY	3481	CTGGTAGCATACAGGCTACGGTGTGGCCAGGGCTCAGGCTCCACTCCATCGTGGAC	3540	Db	4561	CAGATCTCTCTAGTCTTACCATCACTAGCTGCTGAAGAGGCTTACCAGTGGATCAAC	4620
Db	3481	CTGGTAGCATACAGGCTACGGTGTGGCCAGGGCTCAGGCTCCACTCCATCGTGGAC	3540	QY	4621	GAGGACTGTCCACGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC	4680
QY	3541	CAAACTGTGAAGTGTCTCATACGGCTTAAAGCCTACGCTGCACGGGCAACGCCCTCGTGTG	3600	Db	4621	GAGGACTGTCCACGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC	4680
Db	3541	CAAACTGTGAAGTGTCTCATACGGCTTAAAGCCTACGCTGCACGGGCAACGCCCTCGTGTG	3600	QY	4681	ACGGTGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGATTCGCGGGA	4740
QY	3601	TATAGGCTGGAGCCGTTCAAAACGAGGTTATACCAACACACCCCATTAACAAATACATC	3660	Db	4681	ACGGTGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTGCGCGGATTCGCGGGA	4740
Db	3601	TATAGGCTGGAGCCGTTCAAAACGAGGTTATACCAACACACCCCATTAACAAATACATC	3660	QY	4741	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGCGACGGCATCATG	4800
QY	3661	ATGGCATGTGCTGCTGACCTGAGGTGCTCAGGACACCTGGGTGCTGTGAGGCGGA	3720	Db	4741	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGCGACGGCATCATG	4800
Db	3661	ATGGCATGTGCTGCTGACCTGAGGTGCTCAGGACACCTGGGTGCTGTGAGGCGGA	3720	QY	4801	CAAAACACCTGCCCATGTGGAGCACAGATCACCGGACATGTGAAAACCGTTCATGAGG	4860
QY	3721	GTCTTAGCAGCTCTGGCCGCGTATTGCTGACAAACAGGACGCTGTGTCATTGTGGGCAGG	3780	Db	4801	CAAAACACCTGCCCATGTGGAGCACAGATCACCGGACATGTGAAAACCGTTCATGAGG	4860
Db	3721	GTCTTAGCAGCTCTGGCCGCGTATTGCTGACAAACAGGACGCTGTGTCATTGTGGGCAGG	3780	QY	4861	ATCGTGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACATTCCTCCATTAACGCGTAC	4920
QY	3781	ATCATCTTTGTCGGAAGCCGCGCATCATTCGCCAGAGGAGTCTTTTACCGGGAGTTC	3840	Db	4861	ATCGTGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACATTCCTCCATTAACGCGTAC	4920
Db	3781	ATCATCTTTGTCGGAAGCCGCGCATCATTCGCCAGAGGAGTCTTTTACCGGGAGTTC	3840	QY	4921	ACCAAGGCGCCCTGCAACGCTCCCGCGGCAAAATTTATCTAGGGCGCTGTGGCGGTG	4980
QY	3841	GATGAGTAGAAGTGGCGCTCACCTCCCTTACATCGAACAGGGAATGCAGCTCGCC	3900	Db	4921	ACCAAGGCGCCCTGCAACGCTCCCGCGGCAAAATTTATCTAGGGCGCTGTGGCGGTG	4980
Db	3841	GATGAGTAGAAGTGGCGCTCACCTCCCTTACATCGAACAGGGAATGCAGCTCGCC	3900	QY	4981	GCTGCTGAGGAGTACGTGGAGGTTACCGGGGTGGGGGATTTCCACTAGTACGCGGCATG	5040
QY	3901	GAAACAATCAACAGAGAGCAATCGGTTGCTGCAACAGCAGCACCAAGCAGGAGGCT	3960	Db	4981	GCTGCTGAGGAGTACGTGGAGGTTACCGGGGTGGGGGATTTCCACTAGTACGCGGCATG	5040
Db	3901	GAAACAATCAACAGAGAGCAATCGGTTGCTGCAACAGCAGCACCAAGCAGGAGGCT	3960	QY	5041	ACCACTGACAACTGAAAGTGCCTGTGAGGTTCCGGCCCCCGAAATTTCTTACAGAAAGTG	5100
QY	3961	GCTGCTCCGCTGGTGAATCAAGTGGCGGACCTCGAAGCCTTCTGGAAGCGATATG	4020	Db	5041	ACCACTGACAACTGAAAGTGCCTGTGAGGTTCCGGCCCCCGAAATTTCTTACAGAAAGTG	5100
Db	3961	GCTGCTCCGCTGGTGAATCAAGTGGCGGACCTCGAAGCCTTCTGGAAGCGATATG	4020	QY	5101	GATGGGTGCGGTTGCAAGTGTCTCCAGCTGCAACCCCTCTACGGGAGGAGTGC	5160
QY	4021	TGGAATTTCAACAGGAGTATCAATTTAGCAGGCTGTCCACTCTGCTGGCAACCCC	4080	Db	5101	GATGGGTGCGGTTGCAAGTGTCTCCAGCTGCAACCCCTCTACGGGAGGAGTGC	5160
Db	4021	TGGAATTTCAACAGGAGTATCAATTTAGCAGGCTGTCCACTCTGCTGGCAACCCC	4080	QY	5161	ACATTTCTGCTGGCTCAATCAATACCTGTTGGGTGAGTGTGGTCAAGTCCCATGGAGCCGAA	5220
QY	4081	CGATAGCATCACTGATGCAATTCACAGCTTATCAGCAGCCGCTCAGCACCCCAACAT	4140	Db	5161	ACATTTCTGCTGGCTCAATCAATACCTGTTGGGTGAGTGTGGTCAAGTCCCATGGAGCCGAA	5220
Db	4081	CGATAGCATCACTGATGCAATTCACAGCTTATCAGCAGCCGCTCAGCACCCCAACAT	4140	QY	5221	CCGAGCTAGCAGTGTCTCACTTCCATGTCTACCGACCCCTCCCAATTTACCGCGGAGAGC	5280
QY	4141	ACCCCTCTGTTTAAACATCTGGGGGATGGGTGGCGCCCAACTGTCTCTCCAGCGCT	4200	Db	5221	CCGAGCTAGCAGTGTCTCACTTCCATGTCTACCGACCCCTCCCAATTTACCGCGGAGAGC	5280
Db	4141	ACCCCTCTGTTTAAACATCTGGGGGATGGGTGGCGCCCAACTGTCTCTCCAGCGCT	4200	QY	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGTAGCCAG	5340
QY	4201	GCTTCTGCTTTTGGTAGGCGCGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260	Db	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGTAGCCAG	5340
Db	4201	GCTTCTGCTTTTGGTAGGCGCGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260	QY	5341	CTGTCTGGCCCTTCTTGAAGCAACATGCACTACCCGCTCATGCTCCCGGACGCTGAC	5400
QY	4261	AAAGTGTCTTGTGATATTTGGCAGGTTATGAGCAGGGGTGGCAGGCGCTCGTGGCC	4320	Db	5341	CTGTCTGGCCCTTCTTGAAGCAACATGCACTACCCGCTCATGCTCCCGGACGCTGAC	5400
Db	4261	AAAGTGTCTTGTGATATTTGGCAGGTTATGAGCAGGGGTGGCAGGCGCTCGTGGCC	4320	QY	5401	CTCATCGAGGCCAACCTCTCTGCGGCGAGGAGATGGGCGGGAACATACCCCGCTGGAG	5460
QY	4321	TTTAAAGTTCATGAGCGCGGAGATGCTTCCACCGAGGACCTGGTTAAACCTACTCCCTGCT	4380	Db	5401	CTCATCGAGGCCAACCTCTCTGCGGCGAGGAGATGGGCGGGAACATACCCCGCTGGAG	5460
Db	4321	TTTAAAGTTCATGAGCGCGGAGATGCTTCCACCGAGGACCTGGTTAAACCTACTCCCTGCT	4380	QY	5461	TCAGAAATTAAGTGTAGTATTTTGGACTTTTGGAGCTTTTGGAGCTCTTTCGAGCGCTCCAGCGGAGGAGATGAG	5520
QY	4381	ATCCTCTCCCTGGCGGCTGCTGCGGGGTGCTGCGCAGCGATCTGCTGCGGCAC	4440	Db	5461	TCAGAAATTAAGTGTAGTATTTTGGACTTTTGGAGCTTTTGGAGCTCTTTCGAGCGCTCCAGCGGAGGAGATGAG	5520
Db	4381	ATCCTCTCCCTGGCGGCTGCTGCGGGGTGCTGCGCAGCGATCTGCTGCGGCAC	4440	QY	5521	ACGGAGTATCCGTTCCGGCGGAGATCTCTGCGGAGTCCCTGCGAGGTCCAGGAAATTCCTCGAGCGATG	5580
QY	4441	GTGGGCGCAGGGGAGGGGCTGTGCAAGTGTGAACCGGCTGATAGCGTTGGCTTCGCGG	4500	Db	5521	ACGGAGTATCCGTTCCGGCGGAGATCTCTGCGGAGTCCCTGCGAGGTCCAGGAAATTCCTCGAGCGATG	5580
Db	4441	GTGGGCGCAGGGGAGGGGCTGTGCAAGTGTGAACCGGCTGATAGCGTTGGCTTCGCGG	4500	QY	5581	CCCATATGGGACCGCCCGGATTAACACCTCCACTGTTAGAGTCTTGGAGAGACCCGAC	5640
QY	4501	GGTAAACACGCTTCCCGGACGACTATGCTGAGAGCGAGCTCAGCAGCGTGCAT	4560	Db	5581	CCCATATGGGACCGCCCGGATTAACACCTCCACTGTTAGAGTCTTGGAGAGACCCGAC	5640
Db	4501	GGTAAACACGCTTCCCGGACGACTATGCTGAGAGCGAGCTCAGCAGCGTGCAT	4560				

[illegible]

PA	(ALTA/) ALTAMURA S.
PA	(KOCH/) KOCH U.
XX	
XX	Altamura S, Koch U;
PI	
XX	
DR	WPI; 2003-447715/42.
XX	
PT	Treating infections by hepatitis C virus and its related conditions
PT	comprises administering thiosemicarbazone compounds.
XX	
PS	Example 2; Page 9-14; 25pp; English.
XX	
CC	The invention relates to a method of treating or preventing infection by
CC	hepatitis C virus or its related conditions by delaying the onset and
CC	inhibiting replication of hepatitis C virus which comprises administering
CC	thiosemicarbazone compounds. The method is useful for treating or
CC	preventing infection by hepatitis C virus or its related conditions e.g.
CC	liver inflammation, liver failure or cirrhosis, delaying the onset and
CC	inhibiting replication of hepatitis C. The present sequence represents
CC	the hepatitis C virus expression plasmid pHVCNeo17.wt DNA
XX	
SQ	Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
	Query Match 100.0%; Score 7392; DB 9; Length 10690;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 7992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GCCAGCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCCTGTGAGGAATACTTG 60
DB	
QY	61 TCCTTCACGCAGAAGCGTCTAGCCATGGCGTTAGTAGTGTCTGTCAGCCTCCAGGAC 120
DB	
QY	61 TCCTTCACGCAGAAGCGTCTAGCCATGGCGTTAGTAGTGTCTGTCAGCCTCCAGGAC 120
DB	
QY	121 CCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCCGGAATGCCAG 180
DB	
QY	121 CCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCCGGAATGCCAG 180
DB	
QY	181 GACGACCGGCTCTTTCTTGGATCAACCCCGCTCAATGCTGGAGATTTGGCGGTGCCCC 240
DB	
QY	181 GACGACCGGCTCTTTCTTGGATCAACCCCGCTCAATGCTGGAGATTTGGCGGTGCCCC 240
DB	
QY	241 GCGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGCGCTTGTTGCTACTGSCCTGATAGG 300
DB	
QY	241 GCGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGCGCTTGTTGCTACTGSCCTGATAGG 300
DB	
QY	301 GTGCTTCGAGTGCCTCCGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTA AAC 360
DB	
QY	301 GTGCTTCGAGTGCCTCCGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTA AAC 360
DB	
QY	361 CTCAAAGAAAAACCAAGGGCGGCCATGATGTGAACAAGATGGATTCGACGACGAGTCTC 420
DB	
QY	361 CTCAAAGAAAAACCAAGGGCGGCCATGATGTGAACAAGATGGATTCGACGACGAGTCTC 420
DB	
QY	421 CGGCGCTTGGTGGAGAGGCTATTTCGCTATGACTGGGCACAAACAGCAATTCGGCTGCT 480
DB	
QY	421 CGGCGCTTGGTGGAGAGGCTATTTCGCTATGACTGGGCACAAACAGCAATTCGGCTGCT 480
DB	
QY	481 CTGATGCGCGCTGTTCGCGCTGTACAGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540
DB	
QY	481 CTGATGCGCGCTGTTCGCGCTGTACAGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG 540
DB	
QY	541 ACCTGTCCGTCGCCCTGAATGNACTGACGAGGACGAGCGCGCTATCTGTCGCTGGCCA 600
DB	
QY	541 ACCTGTCCGTCGCCCTGAATGNACTGACGAGGACGAGCGCGCTATCTGTCGCTGGCCA 600
DB	
QY	601 CGACGGCGCTTCTTTGCGCAGCTGTGCTCGAGTGTGTCACTGAACGGGAAAGGACTGCG 660
DB	
QY	601 CGACGGCGCTTCTTTGCGCAGCTGTGCTCGAGTGTGTCACTGAACGGGAAAGGACTGCG 660
DB	
QY	661 TGCCTATTGGGCGAAGTGCCGGGGAGGATCTCTCTGTCATCTCACTGTCGTCGGAGA 720
DB	

Db 661 TGCTATTGGCGAAGTCCGGGCGAGGATCTCCCTGTCTCATCTCACTTGTCTCCTCCGAGA 720
QY 721 AAGTATCCATCTGCTGTATGCAATCGCGGCTGTCATACGCTTGATCCGGCTACCTGCC 780
Db 721 AAGTATCCATCTGCTGTATGCAATCGCGGCTGTCATACGCTTGATCCGGCTACCTGCC 780
QY 781 CATTCGACCAACGAGCGAATCGATCGATCGAGGAGCAGCTACTCGGATGGAAGCGGTC 840
Db 781 CATTCGACCAACGAGCGAATCGATCGATCGAGGAGCAGCTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATCAGGATGATCTGGAAGAGAGCATCAGGGGCTCGGCCAGCGAATGTTG 900
Db 841 TTGTGATCAGGATGATCTGGAAGAGAGCATCAGGGGCTCGGCCAGCGAATGTTG 900
QY 901 CAGGCTCAAGGCGGATGCCGAGAGGATCTCGTGTGACCCATGGCGATGCC 960
Db 901 CAGGCTCAAGGCGGATGCCGAGAGGATCTCGTGTGACCCATGGCGATGCC 960
QY 961 GCTTGCAGATATCATGGTGGAAATGGCGCTTTTCTGATTCATCGACTGTGGCGGC 1020
Db 961 GCTTGCAGATATCATGGTGGAAATGGCGCTTTTCTGATTCATCGACTGTGGCGGC 1020
QY 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGCTACCGTGATATGCTGAAGAGC 1080
Db 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGCTACCGTGATATGCTGAAGAGC 1080
QY 1081 TTGGCGGGAATGGGTGACCGCTTCTCGTCTTACCGGTATCGCGCTCCCGATTGCG 1140
Db 1081 TTGGCGGGAATGGGTGACCGCTTCTCGTCTTACCGGTATCGCGCTCCCGATTGCG 1140
QY 1141 AGCGCATCGCTTCTATCGCTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
Db 1141 AGCGCATCGCTTCTATCGCTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTTACTGCG 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAAGTTACTGCG 1260
QY 1261 CGAAGCCGCTTGAATAGGCGGCTGTGCTTGTCTATATGTTATTTTCAACCATATG 1320
Db 1261 CGAAGCCGCTTGAATAGGCGGCTGTGCTTGTCTATATGTTATTTTCAACCATATG 1320
QY 1321 CCGTCTTTTGCAATGTCAGGCGCGGAACTGCGCCCTGCTTCTTGACGAGCATTCCT 1380
Db 1321 CCGTCTTTTGCAATGTCAGGCGCGGAACTGCGCCCTGCTTCTTGACGAGCATTCCT 1380
QY 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGCTGCAAGGAGCA 1440
Db 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGCTGCAAGGAGCA 1440
QY 1441 GTTCTCTGGAAGTCTTGAAGCAAAACACGTCGTAGCGACCCCTTTGAGGCGAGCGG 1500
Db 1441 GTTCTCTGGAAGTCTTGAAGCAAAACACGTCGTAGCGACCCCTTTGAGGCGAGCGG 1500
QY 1501 AACCCCCACCTGCGACAGTGTCTGCGGCCAAAGCCACGTGTATAGATPACCT 1560
Db 1501 AACCCCCACCTGCGACAGTGTCTGCGGCCAAAGCCACGTGTATAGATPACCT 1560
QY 1561 GCAAGCGGCAACACCCAGTGTGAGTTGAGTTGAGTGTGGAAGAGTCAAA 1620
Db 1561 GCAAGCGGCAACACCCAGTGTGAGTTGAGTTGAGTGTGGAAGAGTCAAA 1620
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Db 1621 TGGCTCTCTCAAGCGTATTCACAAAGGCTGAAGGATGCCAGAGGTACCCCATGT 1680
QY 1681 ATGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTGTAGTCAAGTTTAAA 1740
Db 1681 ATGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTGTAGTCAAGTTTAAA 1740
QY 1741 AACGTCTAGGCCCCCGAACCCAGGAGCGTGTCTTTTCTTTTCAAAAACAGTATACC 1800
Db 1741 AACGTCTAGGCCCCCGAACCCAGGAGCGTGTCTTTTCTTTTCAAAAACAGTATACC 1800

QY 1801 ATGGCGCTTATTAGCGGCTACTTCCAAACAGACGAGGCTTACTTGGTGCATCATCACT 1860
Db 1801 ATGGCGCTTATTAGCGGCTACTTCCAAACAGACGAGGCTTACTTGGTGCATCATCACT 1860
QY 1861 AGCTCACAGCGCGGACAGAAACCGAGTTCGAGGGGAGTCCAAAGTGGTCTCCACCGCA 1920
Db 1861 AGCTCACAGCGCGGACAGAAACCGAGTTCGAGGGGAGTCCAAAGTGGTCTCCACCGCA 1920
QY 1921 ACACAATCTTTCTGCGACCTCGCTCAATGGCGTGTGTTGGACTGCTATCATGTGTC 1980
Db 1921 ACACAATCTTTCTGCGACCTCGCTCAATGGCGTGTGTTGGACTGCTATCATGTGTC 1980
QY 1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2040
Db 1981 GGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCAACCAATGTACCAATGTGGAC 2040
QY 2041 CAGGACCTCGTGGCTGGCAAGGCGCCCGCGGGCGCTTCTTGACACCATGCCTGC 2100
Db 2041 CAGGACCTCGTGGCTGGCAAGGCGCCCGCGGGCGCTTCTTGACACCATGCCTGC 2100
QY 2101 GGCGCTCGGACCTTTTACTTGTTCAGAGGSCATGCGATGTCATTCGGGTGCGCGCGG 2160
Db 2101 GGCGCTCGGACCTTTTACTTGTTCAGAGGSCATGCGATGTCATTCGGGTGCGCGCGG 2160
QY 2161 GGCGACAGCAGGGGAGGCTACTCTCCCGAGGCGCTCTCTTCTTGAAGGCTCTTCG 2220
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QY 2221 GGCGCTCGACCTCTGCGCCCTCGGGGACGCTGTGGGATCTTTGGGCTGCGGTGTC 2280
Db 2221 GGCGCTCGACCTCTGCGCCCTCGGGGACGCTGTGGGATCTTTGGGCTGCGGTGTC 2280
QY 2281 ACCGAGGGGTTGCAAGGCGGTGACTTTGTACCGCTGAGTCTATCGAAGACCATATG 2340
Db 2281 ACCGAGGGGTTGCAAGGCGGTGACTTTGTACCGCTGAGTCTATCGAAGACCATATG 2340
QY 2341 CGGTCCCGGCTTCTCAACGCAAACTCGTCCCTCGCGCGGTACCGCAGACATTCAGGTG 2400
Db 2341 CGGTCCCGGCTTCTCAACGCAAACTCGTCCCTCGCGCGGTACCGCAGACATTCAGGTG 2400
QY 2401 GCCCATCTACAGCGCCCTTACTGTTAGGGAAGAGCACTAAGGTGCGGCTGCGTATGCA 2460
Db 2401 GCCCATCTACAGCGCCCTTACTGTTAGGGAAGAGCACTAAGGTGCGGCTGCGTATGCA 2460
QY 2461 GCCCAAGGTTAAGGTGCTTGTCTGAAACCGCTCGCGCGGACCTTAGTGTTCGGG 2520
Db 2461 GCCCAAGGTTAAGGTGCTTGTCTGAAACCGCTCGCGCGGACCTTAGTGTTCGGG 2520
QY 2521 GCGTATATGCTAAGGCATGTTATCGACCTTAACATCAGAACCGGGTAAAGACCATC 2580
Db 2521 GCGTATATGCTAAGGCATGTTATCGACCTTAACATCAGAACCGGGTAAAGACCATC 2580
QY 2581 ACCAGGCTGCGCCCATCAGTACTCAACCTATGCGCAAGTTTCTGCGCAGGTGTTGC 2640
Db 2581 ACCAGGCTGCGCCCATCAGTACTCAACCTATGCGCAAGTTTCTGCGCAGGTGTTGC 2640
QY 2641 TCTGGGGCGCTTATGACATCAATATGATGAGTGCACCTCACTGACTGACCACT 2700
Db 2641 TCTGGGGCGCTTATGACATCAATATGATGAGTGCACCTCACTGACTGACCACT 2700
QY 2701 ATCTGGGATCGGACAGTCTTGGACCAAGCGGAGCGGCTGGAGCGGCTGCTGCTG 2760
Db 2701 ATCTGGGATCGGACAGTCTTGGACCAAGCGGAGCGGCTGGAGCGGCTGCTGCTG 2760
QY 2761 CTCGCCACCGCTACGCTCGGGATCGGTACCGTCCACATCCAAACATCGAGGAGGTG 2820
Db 2761 CTCGCCACCGCTACGCTCGGGATCGGTACCGTCCACATCCAAACATCGAGGAGGTG 2820
QY 2821 GCTCTGTCCGACACTGAGAGAAATCCCTTTTATGGCAAGGACCATCCCATCGAGACATC 2880
Db 2821 GCTCTGTCCGACACTGAGAGAAATCCCTTTTATGGCAAGGACCATCCCATCGAGACATC 2880

2881 AAGGGGGAGGACCTCATTTTCTGCCATTCARAGAGAAATGATGAGCTCGCCGG 2940
2881 AAGGGGGAGGACCTCATTTTCTGCCATTCARAGAGAAATGATGAGCTCGCCGG 2940
2941 AAGCTGTCCGGCTCGGACTCAATGCTGATGATATTAACGGGGCTTGATGATCCGTC 3000
2941 AAGCTGTCCGGCTCGGACTCAATGCTGATGATATTAACGGGGCTTGATGATCCGTC 3000
3001 ATACCAACTAGCGGAGACGCTCATTTGCTGAGCAAGGACGCTTAATGACGGCTTTAC 3060
3001 ATACCAACTAGCGGAGACGCTCATTTGCTGAGCAAGGACGCTTAATGACGGCTTTAC 3060
3061 GCGATTTGCACTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
3061 GCGATTTGCACTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
3121 CTGGACCGACCTTACCTTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
3121 CTGGACCGACCTTACCTTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
3181 CAGCGGCGAGGAGGACTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
3181 CAGCGGCGAGGAGGACTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
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3241 GAACGGCCCTCGGCGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
3301 GCTTGTACGAGCTCACGCGCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA 3360
3301 GCTTGTACGAGCTCACGCGCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA 3360
3361 CCAGGGTTGCCGCTGTCAGGACCATCTGAGTTCTGGGAGAGGCTTTTACAGGCTC 3420
3361 CCAGGGTTGCCGCTGTCAGGACCATCTGAGTTCTGGGAGAGGCTTTTACAGGCTC 3420
3421 ACCACATAGACGCGCTTCTGTCAGGAGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
3421 ACCACATAGACGCGCTTCTGTCAGGAGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
3481 CTGTGATGATACAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540
3481 CTGTGATGATACAGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3540
3541 CAAATGTGGAAGTGTCTCATACGCTAAAGCTTACGCTGACGCGGCTTACGCTGCTGCTG 3600
3541 CAAATGTGGAAGTGTCTCATACGCTAAAGCTTACGCTGACGCGGCTTACGCTGCTGCTG 3600
3601 TATAGGCTGGAGCGCTTCAAAACGAGTTCATCCACACACCCCATACCAATACATC 3660
3601 TATAGGCTGGAGCGCTTCAAAACGAGTTCATCCACACACCCCATACCAATACATC 3660
3661 ATGGCATGATGCTGCGCTCACCTGAGGCTGCTGACGAGGAGGAGGAGGAGGAGGAGGAG 3720
3661 ATGGCATGATGCTGCGCTCACCTGAGGCTGCTGACGAGGAGGAGGAGGAGGAGGAGGAG 3720
3721 GTCTAGAGCTGTGCGCGGATTCCTGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3780
3721 GTCTAGAGCTGTGCGCGGATTCCTGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3780
3781 ATCATCTTGTCCGGAAGCGGCTCATCTCCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 3840
3781 ATCATCTTGTCCGGAAGCGGCTCATCTCCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 3840
3841 GATGAGATGAGAGTGGCTCACCTCTCTTACATCGAAAGGAGGAGGAGGAGGAGGAGGAG 3900
3841 GATGAGATGAGAGTGGCTCACCTCTCTTACATCGAAAGGAGGAGGAGGAGGAGGAGGAG 3900
3901 GAACAAATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3960
3901 GAACAAATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3960
3961 GCTGCTCCCGTGGTGGATCCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4020

3961 GCTGCTCCCGTGGTGGATCCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4020
4021 TGGAAATTTATCAGCGGATACAAATATTAGAGGCTTGTCCACTTCTGCTGGACCC 4080
4021 TGGAAATTTATCAGCGGATACAAATATTAGAGGCTTGTCCACTTCTGCTGGACCC 4080
4081 GCGATAGCATCTGATGGCATTCAGAGCTTATCACCAGCCGCTCACCACCCAAACAT 4140
4081 GCGATAGCATCTGATGGCATTCAGAGCTTATCACCAGCCGCTCACCACCCAAACAT 4140
4141 ACCCTCTCTTTAAATCTCTGGGGGATGGGTGGCCGCCAACTTCTCTCCACGCT 4200
4141 ACCCTCTCTTTAAATCTCTGGGGGATGGGTGGCCGCCAACTTCTCTCCACGCT 4200
4201 GCTTCTGCTTTGCTAGCGCCGCAFCGCTGAGAGCGGCTTGTGGAGCATAGGCTTGG 4260
4201 GCTTCTGCTTTGCTAGCGCCGCAFCGCTGAGAGCGGCTTGTGGAGCATAGGCTTGG 4260
4261 AAGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGCGGCTCGTGCC 4320
4261 AAGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGCGGCTCGTGCC 4320
4321 TTTAAGGTGATGACGCGGAGATGCTCTCCACGAGGACCTGTTAACTTCTCCCTGCT 4380
4321 TTTAAGGTGATGACGCGGAGATGCTCTCCACGAGGACCTGTTAACTTCTCCCTGCT 4380
4381 ATCTCTTCCCTCGGCGCTAGTGTGCTGGGCTGCTGCTGGAGGAGGAGGAGGAGGAGGAG 4440
4381 ATCTCTTCCCTCGGCGCTAGTGTGCTGGGCTGCTGCTGGAGGAGGAGGAGGAGGAGGAG 4440
4441 GTGGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4500
4441 GTGGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4500
4501 GGTAAACACGCTCTCCCGACGCTATGTGCTGAGAGCGAGGCTGACAGGAGGAGGAGGAG 4560
4501 GGTAAACACGCTCTCCCGACGCTATGTGCTGAGAGCGAGGCTGACAGGAGGAGGAGGAG 4560
4561 CAGATCTCTCTAGTCTTACCATCACTGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 4620
4561 CAGATCTCTCTAGTCTTACCATCACTGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 4620
4621 GAGGAGCTCTCCACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4680
4621 GAGGAGCTCTCCACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4680
4681 ACGGTGTTGAGTGTATTTCAAGACCTGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 4740
4681 ACGGTGTTGAGTGTATTTCAAGACCTGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 4740
4741 GTCCCTCTTCTCTCATGTCAAGTGGGTACAGGAGGAGTCTGGCGGGGAGGAGGAGGAGGAG 4800
4741 GTCCCTCTTCTCTCATGTCAAGTGGGTACAGGAGGAGTCTGGCGGGGAGGAGGAGGAGGAG 4800
4801 CAAACACCTGCGCATGTGGAGCAGATCAGCGGAGTGTGAAAGGAGGAGGAGGAGGAGGAGG 4860
4801 CAAACACCTGCGCATGTGGAGCAGATCAGCGGAGTGTGAAAGGAGGAGGAGGAGGAGGAGG 4860
4861 ATCGTGGGCGCTAGGACCTGTAGTAAACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4920
4861 ATCGTGGGCGCTAGGACCTGTAGTAAACGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4920
4921 ACCACGCGCGCTTGCACGCGCTTCCCGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4980
4921 ACCACGCGCGCTTGCACGCGCTTCCCGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4980
4981 GCTGCTGAGAGTACGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
4981 GCTGCTGAGAGTACGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
5041 ACCACTGACAAAGTAAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100

Db 5041 ACCACTGACAAAGTAAAGTCCCGGTGTCAGGTTCCGGCCCCCGAAATCTTTACAGAAAGTG 5100
QY 5101 GATGGGGTGGGTTGCAAGGTACGTCCAGCGTGCAGAAACCCCTCTCTACCGGAGGAGTTC 5160
Db 5101 GATGGGGTGGGTTGCAAGGTACGTCCAGCGTGCAGAAACCCCTCTCTACCGGAGGAGTTC 5160
QY 5161 ACATTCCTGTCGGGCTCAATCAATACCTGGTTGGGTACAGCTCCCATCGCAGGCCGAA 5220
Db 5161 ACATTCCTGTCGGGCTCAATCAATACCTGGTTGGGTACAGCTCCCATCGCAGGCCGAA 5220
QY 5221 CCGGACGTAGCTGCTCACTCCATGCTCACCGACCCCTCCACATTAAGCGGGAGAG 5280
Db 5221 CCGGACGTAGCTGCTCACTCCATGCTCACCGACCCCTCCACATTAAGCGGGAGAG 5280
QY 5281 GCTAAGCGTAGCTGCTGCTGAGGAGGATCTCCCGCTCTGTCAGCTCATCAGCTAGCCAG 5340
Db 5281 GCTAAGCGTAGCTGCTGCTGAGGAGGATCTCCCGCTCTGTCAGCTCATCAGCTAGCCAG 5340
QY 5341 CTGCTGCGCCCTTCCCTTGAAGCAATGCTACCTACCGCTCATGCTCCCGGAGCGTGC 5400
Db 5341 CTGCTGCGCCCTTCCCTTGAAGCAATGCTACCTACCGCTCATGCTCCCGGAGCGTGC 5400
QY 5401 CTCATCGAGGCCAACCTCTGTCGGGCGAGGAGATGGGCGGAAACATCACCCGCTGGAG 5460
Db 5401 CTCATCGAGGCCAACCTCTGTCGGGCGAGGAGATGGGCGGAAACATCACCCGCTGGAG 5460
QY 5461 TCAGAAATAAGGTAGTAAATTTGGACTCTTTTCGAGCGCTCCAGCGGAGGAGATGAG 5520
Db 5461 TCAGAAATAAGGTAGTAAATTTGGACTCTTTTCGAGCGCTCCAGCGGAGGAGATGAG 5520
QY 5521 AGGGAAGTATCCGTCGCGCGAGATCTCGGAGTCCAGAAATTCCTTCGAGCGATG 5580
Db 5521 AGGGAAGTATCCGTCGCGCGAGATCTCGGAGTCCAGAAATTCCTTCGAGCGATG 5580
QY 5581 CCCATATGGGACGCCCGGATTAACACCTCCACTGTTAGAGTCTCTGAAAGAACCCGAG 5640
Db 5581 CCCATATGGGACGCCCGGATTAACACCTCCACTGTTAGAGTCTCTGAAAGAACCCGAG 5640
QY 5641 TACGTCCCTCAAGTGTGTACACGGGTGTCATGTCGCGCTCCAGGCCCTCCGATACCA 5700
Db 5641 TACGTCCCTCAAGTGTGTACACGGGTGTCATGTCGCGCTCCAGGCCCTCCGATACCA 5700
QY 5701 CCTCCAGGAGGAGAGACGGTGTCTGTGTCAGAAATCTACCGTGTCTTCTGCTTGGCG 5760
Db 5701 CCTCCAGGAGGAGAGACGGTGTCTGTGTCAGAAATCTACCGTGTCTTCTGCTTGGCG 5760
QY 5761 GAGTCCGCCAACAAGACCTTCGCGAGCTCCGAAATCTGTCGGCGCTCGACGCGGACCGCA 5820
Db 5761 GAGTCCGCCAACAAGACCTTCGCGAGCTCCGAAATCTGTCGGCGCTCGACGCGGACCGCA 5820
QY 5821 ACGGCTCTCTGACAGCCCTTCGACGCGGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 5880
Db 5821 ACGGCTCTCTGACAGCCCTTCGACGCGGAGTCCGAGTCCGAGTCCGAGTCCGAGTCCG 5880
QY 5881 TCCTCCATGCCCCCTTGAAGGGGAGCCGGGATCCCATCTCAGCGACGGTCTTGG 5940
Db 5881 TCCTCCATGCCCCCTTGAAGGGGAGCCGGGATCCCATCTCAGCGACGGTCTTGG 5940
QY 5941 TCTACCGTAAGCGAGGAGGCTAGTAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6000
Db 5941 TCTACCGTAAGCGAGGAGGCTAGTAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6000
QY 6001 ACAGGCGCTGATACGCGCATCGCTGCGAGGAAACCAAGCTGCCCATCAATGCACTG 6060
Db 6001 ACAGGCGCTGATACGCGCATCGCTGCGAGGAAACCAAGCTGCCCATCAATGCACTG 6060
QY 6061 AGCAACTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6120
Db 6061 AGCAACTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6120
QY 6121 CTGCGGAGAGAGAGTCACTTTGACAGCTGACAGTCTGAGTCTGAGTCTGAGTCTGAGT 6180
Db 6121 CTGCGGAGAGAGAGTCACTTTGACAGCTGACAGTCTGAGTCTGAGTCTGAGTCTGAGT 6180

QY 6181 GTGCTCAAGAGATGAAGCGAAGGCGTCCACAGTTAAGCTAACTTCTATCCGTGGAG 6240
Db 6181 GTGCTCAAGAGATGAAGCGAAGGCGTCCACAGTTAAGCTAACTTCTATCCGTGGAG 6240
QY 6241 GAAGCCCTGTAAGCTGACGCCGCCACATTCGGCCAGATCTAAATTTGGCTATGCGGCAAG 6300
Db 6241 GAAGCCCTGTAAGCTGACGCCGCCACATTCGGCCAGATCTAAATTTGGCTATGCGGCAAG 6300
QY 6301 GAGCTCCGAAACCTATCCAGCAAGGCCGTTAAACCATCCGCTCCGTGTTGGAAGGACTTG 6360
Db 6301 GAGCTCCGAAACCTATCCAGCAAGGCCGTTAAACCATCCGCTCCGTGTTGGAAGGACTTG 6360
QY 6361 CTGGAAGACACTGAGACCAATTTGACACCAATCATGGCAAAATGAGGTTTTCTGC 6420
Db 6361 CTGGAAGACACTGAGACCAATTTGACACCAATCATGGCAAAATGAGGTTTTCTGC 6420
QY 6421 GTCCCAACAGAGAGAGGCCGCGCAAGCCAGCTCGGCTTATCGTATTCACAGATTTGGG 6480
Db 6421 GTCCCAACAGAGAGAGGCCGCGCAAGCCAGCTCGGCTTATCGTATTCACAGATTTGGG 6480
QY 6481 GTTCGTGTGTGCGAGAAATGGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGCTG 6540
Db 6481 GTTCGTGTGTGCGAGAAATGGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGCTG 6540
QY 6541 ATGGGCTCTTCATACCGAATTCCTCTCTGACAGCGGCTCGAGTTCCTGCTGAAT 6600
Db 6541 ATGGGCTCTTCATACCGAATTCCTCTCTGACAGCGGCTCGAGTTCCTGCTGAAT 6600
QY 6601 GCCTGGAAGCGAAGAAATGGCCCTATGGCTTCGATATGACACCCGCTGTTTCACTCA 6660
Db 6601 GCCTGGAAGCGAAGAAATGGCCCTATGGCTTCGATATGACACCCGCTGTTTCACTCA 6660
QY 6661 ACGGTCACTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGTTGACTTGGCC 6720
Db 6661 ACGGTCACTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGTTGACTTGGCC 6720
QY 6721 CCCGAGCGACAGAGGCGAATGAGTCTCACAGAGCGGCTTTACATCGGGGCCCCCTG 6780
Db 6721 CCCGAGCGACAGAGGCGAATGAGTCTCACAGAGCGGCTTTACATCGGGGCCCCCTG 6780
QY 6781 ACTAATTTAAAGGCGAAGTCCGCTATCGCGGTGCGCGGAGCGGTGTAAGTCA 6840
Db 6781 ACTAATTTAAAGGCGAAGTCCGCTATCGCGGTGCGCGGAGCGGTGTAAGTCA 6840
QY 6841 ACCAGCTCGGTAATACCTTCACATGTTACTTGAAGCGCTGCGGCTGCGGCTGCGGCTGCG 6900
Db 6841 ACCAGCTCGGTAATACCTTCACATGTTACTTGAAGCGCTGCGGCTGCGGCTGCGGCTGCG 6900
QY 6901 AAGCTCCAGGACTGACAGTCTGCTGAGGAGACGACCTTGTGTTATCTGTGAAAGC 6960
Db 6901 AAGCTCCAGGACTGACAGTCTGCTGAGGAGACGACCTTGTGTTATCTGTGAAAGC 6960
QY 6961 GCGGGACCCCAAGAGGAGGAGCGCTTACGGGCTTACGGAGGCTATGATAGATC 7020
Db 6961 GCGGGACCCCAAGAGGAGGAGCGCTTACGGGCTTACGGAGGCTATGATAGATC 7020
QY 7021 TGTGCCCCCTTGGGAGCCCGCCAAACAGAAATACGACTTGGAGTTGATAACATCATGC 7080
Db 7021 TGTGCCCCCTTGGGAGCCCGCCAAACAGAAATACGACTTGGAGTTGATAACATCATGC 7080
QY 7081 TCTCCATGTTGTCACTCGGCGACGATCATCTGGCAAAAGGCTGACTATCTCACCCGT 7140
Db 7081 TCTCCATGTTGTCACTCGGCGACGATCATCTGGCAAAAGGCTGACTATCTCACCCGT 7140
QY 7141 GACCCACCAACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACTCCAGTCAAT 7200
Db 7141 GACCCACCAACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACTCCAGTCAAT 7200
QY 7201 TCTGCTAGGCAACATCATCATGATGATGCGCCACCTTGTGGGCAAGGATGATCCTGATG 7260
Db 7201 TCTGCTAGGCAACATCATCATGATGATGCGCCACCTTGTGGGCAAGGATGATCCTGATG 7260

QY	7261	ACTCATTTCTTCTCCATCCTTCTAGCTCAGGAACAACATTGAAAAGCCCTAGATTGTCAAG	7320
Db	7261		7320
Db	7261	ACTCATTTCTTCTCCATCCTTCTAGCTCAGGAACAACATTGAAAAGCCCTAGATTGTCAAG	7320
QY	7321	AUTCAGGGGCCCTTGTTTACTCCATTGAGCCAATTGACCTACCTCAGATCATTTCAACGACTC	7380
Db	7321		7380
QY	7381	CATGGCCCTTAGCGCATTTTTCACCTCCATAGTACTCTCCAGGTGAGATCAATAGAGGTGGCT	7440
Db	7381		7440
QY	7441	TCATGCCTCAGGAAACTTTGGGGTACCGCCCTTGGAGATCTGCGAGTCTGGAGACATCGGGCCAGAAGT	7500
Db	7441		7500
QY	7501	GTCGCGCTTAGGCTACTGTCCCAGGGGGGAGGGCTGCCACATTGTGGGAAAGTACCTCTTC	7560
Db	7501		7560
QY	7561	AACTGGGCGAGTAAGGACCAAGCTCAAACCTCACCTCCCAATCCCGGCTCGCTCCCAAGTTGGAT	7620
Db	7561		7620
QY	7621	TTATCCAGCTGTTTCGTTGCTGTTTACAGCGGGGGAGACATAATACAGCCTGTCTCGT	7680
Db	7621		7680
QY	7681	GCCCGAACCCGCTGGTTCAAGTGTCCTACTCTTCTAGGGGTAGGCATCTAT	7740
Db	7681		7740
QY	7741	CTACTCCCCAACCAGTAAAGCGGAGCTAAACACTCCAGGCCAATAGGCCCATCTCTGTTTT	7800
Db	7741		7800
QY	7801	TTTTCCCTTTTTTTTTTTCTTT	7860
Db	7801		7860
QY	7861	TTTTTCCCTTTTTTTTTTTCTTT	7920
Db	7861		7920
QY	7921	TAGCTGTGAAGGTCGGTGAGCGCTTGACTGCAGAGAGTCTCATACTTGGCCTCTCTGC	7980
Db	7921		7980
QY	7981	AGATCAAGTACT	7992
Db	7981		7992
RESULT 4			
ADC83762			
ID	ADC83762 standard; DNA; 10690 BP.		
XX	AC ADC83762;		
XX	DT		
XX	01-JAN-2004 (first entry)		
XX	pHCVNeo17.wt plasmid containing an HCV bicistronic replicon.		
XX	Hepatitis C virus; thiosemicarbazone;		
KW	4-(cinnaamoyl)benzaldehyde thiosemicarbazone; RHEPLISA; Ia; hepatitis C;		
KW	HCV replication system; bicistronic RNA replicon;		
KW	neomycin phosphotransferase; human hepatoma cell line; Huh-7;		
KW	neomycin sulphate; G418; pHCVNeo17.wt; replicon 1377neo/NS3-3./wt.;		
KW	hepatotropic; virucide; antiinflammatory; ds.		
OS	Synthetic.		
OS	Unidentified.		
OS	Hepatitis C virus.		

Db 301 GTGCTTGCAGTGTCCCGGAGGTCTCGTAGACCGTGCACTGAGCACGAATCCTAAAC 360
QY 361 CTCAGAGAAAAACAAGAGCGGCCCATGATGAACAAGATGGATTGCACGCGAGTTCTC 420
Db 361 CTCAGAGAAAAACAAGAGCGGCCCATGATGAACAAGATGGATTGCACGCGAGTTCTC 420
QY 421 CGGCGCTTGGGTGGAGAGGCTATTGGCTATGACTGAGTGGGACAAACAGCAATCGGCTGCT 480
Db 421 CGGCGCTTGGGTGGAGAGGCTATTGGCTATGACTGAGTGGGACAAACAGCAATCGGCTGCT 480
QY 481 CTGATGCGCGGTGTTCGCGCTGTGACGCGAGGGGGCGCCGGTCTTTTGTCAAGACCG 540
Db 481 CTGATGCGCGGTGTTCGCGCTGTGACGCGAGGGGGCGCCGGTCTTTTGTCAAGACCG 540
QY 541 ACCTGTCCGGTCCCTGAATGAATCTGAGGACGAGGCGCGGCTATCGTGGCTGGCCA 600
Db 541 ACCTGTCCGGTCCCTGAATGAATCTGAGGACGAGGCGCGGCTATCGTGGCTGGCCA 600
QY 601 CGACGGGCGCTTCCTTTCGCGAGCTGTGCTCGAGCTTGTCTACTGAAGCGGGAAGGACTGCG 660
Db 601 CGACGGGCGCTTCCTTTCGCGAGCTGTGCTCGAGCTTGTCTACTGAAGCGGGAAGGACTGCG 660
QY 661 TGCTATTGGGCGAAGTGCCTGGGCGAGGATCTCTGTGCTATCTCACCTTGTCTCCGCGGAGA 720
Db 661 TGCTATTGGGCGAAGTGCCTGGGCGAGGATCTCTGTGCTATCTCACCTTGTCTCCGCGGAGA 720
QY 721 AAGTATCCATCATGCTGATGCAATGCGGCGCTGCATACGCTTGTATCCGGTACTGCTGCC 780
Db 721 AAGTATCCATCATGCTGATGCAATGCGGCGCTGCATACGCTTGTATCCGGTACTGCTGCC 780
QY 781 CATTCGACCAACAAGCGAAACATCCATCGAGGAGCAGTACTCGGATGGAAGCGGTC 840
Db 781 CATTCGACCAACAAGCGAAACATCCATCGAGGAGCAGTACTCGGATGGAAGCGGTC 840
QY 841 TTGTGATPAGGATGATCTGGAACGAAGACATPAGGGCTCGCGCCAGCGACGACTGTTGCG 900
Db 841 TTGTGATPAGGATGATCTGGAACGAAGACATPAGGGCTCGCGCCAGCGACGACTGTTGCG 900
QY 901 CCAGGCTCAAGGCGGATGCGCGACGCGAGGATCTCGTGTGACCCATGCGGATGCT 960
Db 901 CCAGGCTCAAGGCGGATGCGCGACGCGAGGATCTCGTGTGACCCATGCGGATGCT 960
QY 961 GCTTGCAGATATCATGTTGGAATGCGCGCTTTCTGGAATCATGACTGTGCGCGGC 1020
Db 961 GCTTGCAGATATCATGTTGGAATGCGCGCTTTCTGGAATCATGACTGTGCGCGGC 1020
QY 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATTTGCTGAAGAGC 1080
Db 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATTTGCTGAAGAGC 1080
QY 1081 TTGGCGGGAATGGGCTGACCGCTTCTCGTGTGTTTACGGTATGCGCGCTCCCGATTGCG 1140
Db 1081 TTGGCGGGAATGGGCTGACCGCTTCTCGTGTGTTTACGGTATGCGCGCTCCCGATTGCG 1140
QY 1141 AGCGCATCGCTTCTATCGCTTCTTGAACAGTCTTCTGAGTTTAAACAGACACAAG 1200
Db 1141 AGCGCATCGCTTCTATCGCTTCTTGAACAGTCTTCTGAGTTTAAACAGACACAAG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTTACAGTTTCTGCG 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTTACAGTTTCTGCG 1260
QY 1261 CGAAGCGGCTTGAATTAAGGCGCGGTGCGCTTGTCTATATGTTATTTTCCACCATTTG 1320
Db 1261 CGAAGCGGCTTGAATTAAGGCGCGGTGCGCTTGTCTATATGTTATTTTCCACCATTTG 1320
QY 1321 CGCTCTTTTGGCAATGTAGGGCCCGGAACCTGGCCCTGTCTCTGAGCAGCATTCCT 1380
Db 1321 CGCTCTTTTGGCAATGTAGGGCCCGGAACCTGGCCCTGTCTCTGAGCAGCATTCCT 1380
QY 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTGAATGCTGAGGAGCA 1440
Db 1381 AGGGGTCTTTCCTCTCGCCAAAGGAATGCAAGGTCTGTGAATGCTGAGGAGCA 1440

QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAACGTCGTGTAGCAGCCCTTTGAGGACGGG 1500
Db 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAACGTCGTGTAGCAGCCCTTTGAGGACGGG 1500
QY 1501 AACCCGCCACTCGGACAGGTCCTCTGGGCGAAAGCCAGTGATTAAGATPACACCT 1560
Db 1501 AACCCGCCACTCGGACAGGTCCTCTGGGCGAAAGCCAGTGATTAAGATPACACCT 1560
QY 1561 GCAAGCGGCGCAACCCAGTGCACGTTGTGAGTTGGATAGTTGGAAGAGGTCAAA 1620
Db 1561 GCAAGCGGCGCAACCCAGTGCACGTTGTGAGTTGGATAGTTGGAAGAGGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAGGTACCCCAATTGT 1680
Db 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAGGTACCCCAATTGT 1680
QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTGTAGTCGAGGTTAAAA 1740
Db 1681 ATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTGTAGTCGAGGTTAAAA 1740
QY 1741 AACGTCTAGGCCCCCGAAACACGCGGACGTTTCTTTTGAAGAAACACCATATACC 1800
Db 1741 AACGTCTAGGCCCCCGAAACACGCGGACGTTTCTTTTGAAGAAACACCATATACC 1800
QY 1801 ATGGCGCTATTACGGCTACTTCCAAACAGCGGAGGCTACTTGGTGCATCATCACT 1860
Db 1801 ATGGCGCTATTACGGCTACTTCCAAACAGCGGAGGCTACTTGGTGCATCATCACT 1860
QY 1861 AGCTCTACAGCGCGGACAGGAACAGGTGCGAGGGGAGGTCCTAAGTGGTCTCCACCGCA 1920
Db 1861 AGCTCTACAGCGCGGACAGGAACAGGTGCGAGGGGAGGTCCTAAGTGGTCTCCACCGCA 1920
QY 1921 ACACAACTTTTCTGGCGACCTCGTCAATGCGGTGCTGAGTCTATCATGCTGCC 1980
Db 1921 ACACAACTTTTCTGGCGACCTCGTCAATGCGGTGCTGAGTCTATCATGCTGCC 1980
QY 1981 GGCTCAAGAACCTTGGCGGCCAAAGGGCCCAATCACCCAAATGTACCAAAATGTGGAC 2040
Db 1981 GGCTCAAGAACCTTGGCGGCCAAAGGGCCCAATCACCCAAATGTACCAAAATGTGGAC 2040
QY 2041 CAGGACCTCGTGCCTGGCAAGCGCCCCCGGGCGGCTTCTTTGACACCAATGCACCTGC 2100
Db 2041 CAGGACCTCGTGCCTGGCAAGCGCCCCCGGGCGGCTTCTTTGACACCAATGCACCTGC 2100
QY 2101 GGCACTCGGACCTTTACTTGGTCAAGGACATGCCGATGCTTCCGGTGCCTGCTGC 2160
Db 2101 GGCACTCGGACCTTTACTTGGTCAAGGACATGCCGATGCTTCCGGTGCCTGCTGC 2160
QY 2161 GGCGACAGGAGGAGGCTTCTTCCCGCGGCGCTCTCTCTTGAAGGGCTCTTCG 2220
Db 2161 GGCGACAGGAGGAGGAGGCTTCTTCCCGCGGCGCTCTCTCTTGAAGGGCTCTTCG 2220
QY 2221 GGCGGTCTACTGCTTCCCGCTCGGGCAGCTGTGGGATCTTTTGGGTGCGGTGTC 2280
Db 2221 GGCGGTCTACTGCTTCCCGCTCGGGCAGCTGTGGGATCTTTTGGGTGCGGTGTC 2280
QY 2281 ACCGAGGGGTTGCGAAGCGGTGGAATTTGTACCCGTCGAGTCTATGGAACACATATG 2340
Db 2281 ACCGAGGGGTTGCGAAGCGGTGGAATTTGTACCCGTCGAGTCTATGGAACACATATG 2340
QY 2341 CGGTCCCGGTCTTTCACGACAACTCGTCCCTCGGCGGTACCGCAGACATTCAGGTG 2400
Db 2341 CGGTCCCGGTCTTTCACGACAACTCGTCCCTCGGCGGTACCGCAGACATTCAGGTG 2400
QY 2401 GCCATCTACAGCCCTTACTGTAGCGCAAGACACTAAGGTGCGGTGCGTATGCA 2460
Db 2401 GCCATCTACAGCCCTTACTGTAGCGCAAGACACTAAGGTGCGGTGCGTATGCA 2460
QY 2461 GCCAAGGATTAAGGTGCTTCTCTGAACCGCTCCGTCGCCGCCACCTAGTTTCGG 2520
Db 2461 GCCAAGGATTAAGGTGCTTCTCTGAACCGCTCCGTCGCCGCCACCTAGTTTCGG 2520

QY	2521	GGGTATATGCTTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGGTAAAGCAATC	2580	3601	TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACACACCCCATAAACCAATACATC	3660	
DB	2521	GGGTATATGCTTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGGTAAAGCAATC	2580	QY	3661	ATGGCATGATGTGGCTGACCTGGAGGTGCTCAGAGCACTGGTGTCTGGTAGGCGGA	3720
QY	2581	ACCACGGGTGCCCCCATCAGCTACTCCACCTAATGGAAGATTTCTTTGCCGACGGTGGTGC	2640	DB	3661	ATGGCATGATGTGGCTGACCTGGAGGTGCTCAGAGCACTGGTGTCTGGTAGGCGGA	3720
DB	2581	ACCACGGGTGCCCCCATCAGCTACTCCACCTAATGGAAGATTTCTTTGCCGACGGTGGTGGC	2640	QY	3721	GTCTAGCAGCTCTGGCGCGTATTGCCCTGACAAACAGGACGGTGTCTAATGTGGGACGG	3780
QY	2641	TCGTGGGGGCGCCTATGACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700	DB	3721	GTCTAGCAGCTCTGGCGCGTATTGCCCTGACAAACAGGACGGTGTCTAATGTGGGACGG	3780
DB	2641	TCGTGGGGGCGCCTATGACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCACT	2700	QY	3781	ATCATCTTGTCCGAAAGCCGCCATCATTTCCCGACAGGGAAGTCTTTACCGGGAGTTC	3840
QY	2701	ATCTGGGATCGGACAGTCTCGGACCAAGCGGACCGGCTGGAGCGGACCTCGTCTGTG	2760	DB	3781	ATCATCTTGTCCGAAAGCCGCCATCATTTCCCGACAGGGAAGTCTTTACCGGGAGTTC	3840
DB	2701	ATCTGGGATCGGACAGTCTCGGACCAAGCGGACCGGCTGGAGCGGACCTCGTCTGTG	2760	QY	3841	GATGAGATGGAAGAGTGGCGCTCACACCTCCCTTTACATCGAACGAGGAATGACAGCTCGCC	3900
QY	2761	CTCGCCACCGCTACGCTCGGATCGGTACCGTGCACATCCAAACATCGAGGAGTG	2820	DB	3841	GATGAGATGGAAGAGTGGCGCTCACACCTCCCTTTACATCGAACGAGGAATGACAGCTCGCC	3900
DB	2761	CTCGCCACCGCTACGCTCGGATCGGTACCGTGCACATCCAAACATCGAGGAGTG	2820	QY	3901	GAAATTTCAACAGAGGCAATCGGGTGTCTGMAACAGCCACCAAGCAAGCGGAGGCT	3960
QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880	DB	3901	GAAATTTCAACAGAGGCAATCGGGTGTCTGMAACAGCCACCAAGCAAGCGGAGGCT	3960
DB	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880	QY	3961	GCTGCTCCGCTGTGGAATCCAAAGTGGCGGACCTCGAAGCTCTTCTGGGCGAAGCATATG	4020
QY	2881	AAGGGGGAGGACCTCATTTTCTGCAATTCGAAGAAATGTGATGAGTTCGCGCG	2940	DB	3961	GCTGCTCCGCTGTGGAATCCAAAGTGGCGGACCTCGAAGCTCTTCTGGGCGAAGCATATG	4020
DB	2881	AAGGGGGAGGACCTCATTTTCTGCAATTCGAAGAAATGTGATGAGTTCGCGCG	2940	QY	4021	TGGAATTTTCAACAGAGGCAATCGGGTGTCTGMAACAGCCACCAAGCAAGCGGAGGCT	4080
QY	2941	AAGCTGTCCGCGCTCGGACTCAATGTGTAGCATATTACGGGGCTTGTATGTATCGGTC	3000	DB	4021	TGGAATTTTCAACAGAGGCAATCGGGTGTCTGMAACAGCCACCAAGCAAGCGGAGGCT	4080
DB	2941	AAGCTGTCCGCGCTCGGACTCAATGTGTAGCATATTACGGGGCTTGTATGTATCGGTC	3000	QY	4081	GCGATAGCATCATGATGGCATTCACAGCTCTATCACAGCCCGCTCACACCCAAACAT	4140
QY	3001	ATACCAACTAGCGAGAGCTCATTTGTAGTATTAATACGGGCTTATATGACGGGCTTACC	3060	DB	4081	GCGATAGCATCATGATGGCATTCACAGCTCTATCACAGCCCGCTCACACCCAAACAT	4140
DB	3001	ATACCAACTAGCGAGAGCTCATTTGTGTAGTATTAATACGGGCTTATATGACGGGCTTACC	3060	QY	4141	ACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGCT	4200
QY	3061	GGCGATTTGCACTCAGTGATCGACTGCAATACATGTGTACCAACCGGCTTAAATGACGGGCTTACC	3120	DB	4141	ACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGCT	4200
DB	3061	GGCGATTTGCACTCAGTGATCGACTGCAATACATGTGTACCAACCGGCTTAAATGACGGGCTTACC	3120	QY	4201	GCTTCTGCTTTCGTAGGCGCGGACATCGCTGGAGCGGCTGTGGCAGCATAGGCGCTTGGG	4260
QY	3121	CTGGACCGGACTTCAACATTTAGACAGCAGCCGTGCCCAAGACGCGGTTGACGCTCG	3180	DB	4201	GCTTCTGCTTTCGTAGGCGCGGACATCGCTGGAGCGGCTGTGGCAGCATAGGCGCTTGGG	4260
DB	3121	CTGGACCGGACTTCAACATTTAGACAGCAGCCGTGCCCAAGACGCGGTTGACGCTCG	3180	QY	4261	AAGTGTCTGTGGATATTTTGGCAGGCTATGGAGCAGGGGTGGAGCGCGCTCGTGGCC	4320
QY	3181	CAGCGCGGAGGACGAGTGGTATGAGGAGTGGGCAATTTACAGTTTGTGACTCCAGGA	3240	DB	4261	AAGTGTCTGTGGATATTTTGGCAGGCTATGGAGCAGGGGTGGAGCGCGCTCGTGGCC	4320
DB	3181	CAGCGCGGAGGACGAGTGGTATGAGGAGTGGGCAATTTACAGTTTGTGACTCCAGGA	3240	QY	4321	TTTAAAGTTCATGAGCGCGGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT	4380
QY	3241	GAAAGGCTCGGGCATGTTCTGAGTTCCTCGTTCGTGCGAGTGTATGACGCGGGCTGT	3300	DB	4321	TTTAAAGTTCATGAGCGCGGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT	4380
DB	3241	GAAAGGCTCGGGCATGTTCTGAGTTCCTCGTTCGTGCGAGTGTATGACGCGGGCTGT	3300	QY	4381	ATCCTCTCCCTTGGCGCGCTAGTGTGGGGTGTGTGGCAGCCATCTCGTGGCGAC	4440
QY	3301	GCTTGTGTAGAGTCAAGCGCGCGGAGACCTCAGTTAGGTTGCGGGCTTACTAAACACA	3360	DB	4381	ATCCTCTCCCTTGGCGCGCTAGTGTGGGGTGTGTGGCAGCCATCTCGTGGCGAC	4440
DB	3301	GCTTGTGTAGAGTCAAGCGCGCGGAGACCTCAGTTAGGTTGCGGGCTTACTAAACACA	3360	QY	4441	GTGGGCGGAGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTCGCTTCGCGG	4500
QY	3361	CCAGGGTTCGCGCTCTGCCAGGACCATCTGAGTTCGTGGAGAGGCTTTACAGGCGCTC	3420	DB	4441	GTGGGCGGAGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTCGCTTCGCGG	4500
DB	3361	CCAGGGTTCGCGCTCTGCCAGGACCATCTGAGTTCGTGGAGAGGCTTTACAGGCGCTC	3420	QY	4501	GGTAAACAGCTCTCCCGGAGGCTATGTGCCCTGAGAGCGAGCTGACAGCGTGTCACT	4560
QY	3421	ATCCATAGACGCGGCTTCTGAGTTCGTGGAGAGGCTTTACAGGCGCTC	3480	DB	4501	GGTAAACAGCTCTCCCGGAGGCTATGTGCCCTGAGAGCGAGCTGACAGCGTGTCACT	4560
DB	3421	ATCCATAGACGCGGCTTCTGAGTTCGTGGAGAGGCTTTACAGGCGCTC	3480	QY	4561	CAGATCTCTCTAGTCTTACCATCTCAGCTCTCGAAGAGGCTTCCAGTGGATCAAC	4620
QY	3481	CTGGTATGACATCAGGCTAGGCTAGGCTCAGGCTCCAGCTCCACTCGTGGGAC	3540	DB	4561	CAGATCTCTCTAGTCTTACCATCTCAGCTCTCGAAGAGGCTTCCAGTGGATCAAC	4620
DB	3481	CTGGTATGACATCAGGCTAGGCTAGGCTCAGGCTCCAGCTCCACTCGTGGGAC	3540	QY	4621	GAGGACTGTCTCCAGCGGATGCTCCGGCTCGTGGCTTAAGAGTGTGGGATTTGGATATGC	4680
QY	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAAGCCATACGCTGACCGGCGCAAGCCCTGCTG	3600	DB	4621	GAGGACTGTCTCCAGCGGATGCTCCGGCTCGTGGCTTAAGAGTGTGGGATTTGGATATGC	4680
DB	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAAGCCATACGCTGACCGGCGCAAGCCCTGCTG	3600	QY	4681	ACGGTGTGACTGATTTCAAGACTCGGCTCCAGTCCAAAGCTCTCTGCGCGGATTTGCCGGGA	4740
QY	3601	TATAGGCTGGAGCGGTTCAAAACGAGGTTACTATACACACCCCATAAACCAATACATC	3660				

6901 AAGCTCCAGGACTGACGAGTCTCGTATGCGGAGACGACCTTGTCTATCTGTGAAGC 6960
6901 AAGCTCCAGGACTGACGAGTCTCGTATGCGGAGACGACCTTGTCTATCTGTGAAGC 6960
6961 GCGGGGACCCAAAGAGGAGCGAGCGCTTACGAGGCTTACGAGGCTATGACTAGATAC 7020
6961 GCGGGGACCCAAAGAGGAGCGAGCGCTTACGAGGCTTACGAGGCTATGACTAGATAC 7020
7021 TCTGCCCCCTGCGGAGCCCGCCAAACAGAAATACGAGTTGGAGTTGATACATCATGCG 7080
7021 TCTGCCCCCTGCGGAGCCCGCCAAACAGAAATACGAGTTGGAGTTGATACATCATGCG 7080
7081 TCTTCCAAATGTCTAGTCCGCGACGATGATCTGGGAAAGGCTTACTCTACCCCGT 7140
7081 TCTTCCAAATGTCTAGTCCGCGACGATGATCTGGGAAAGGCTTACTCTACCCCGT 7140
7141 GACCCACACCCCTTCCGCGGGTGGTGGGAGACAGCTAGACACACTCCAGTCAAT 7200
7141 GACCCACACCCCTTCCGCGGGTGGTGGGAGACAGCTAGACACACTCCAGTCAAT 7200
7201 TCTGCTAGGCAACATCATATGATGATGCGCCACCTTGTGGCAAGGATGATCCTGATG 7260
7201 TCTGCTAGGCAACATCATATGATGATGCGCCACCTTGTGGCAAGGATGATCCTGATG 7260
7261 ACTCATTTCTTCCATCTTCTAGCTCAGGAACAATCTTGAAGAGCCCTAGATTTGTCAG 7320
7261 ACTCATTTCTTCCATCTTCTAGCTCAGGAACAATCTTGAAGAGCCCTAGATTTGTCAG 7320
7321 ATCTAGGGGCTTACTCCATGAGCCACTTGAACCTACTCAGATCAATCAACGACTC 7380
7321 ATCTAGGGGCTTACTCCATGAGCCACTTGAACCTACTCAGATCAATCAACGACTC 7380
7381 CATGCGCTTACGCAATTTTCACTCCATGATTTACTTCTCCAGTGAGATCAATAGGCTGCT 7440
7381 CATGCGCTTACGCAATTTTCACTCCATGATTTACTTCTCCAGTGAGATCAATAGGCTGCT 7440
7441 TCATGCTCAGGAACATTTGGGCTACCGCTTGGAGTCTGGAGACATCGGCGCAGAGT 7500
7441 TCATGCTCAGGAACATTTGGGCTACCGCTTGGAGTCTGGAGACATCGGCGCAGAGT 7500
7501 GTCCGCGTACTGCTTCCAGGGGAGGCTGCGCACTTGTGGCAAGTACCTCTTC 7560
7501 GTCCGCGTACTGCTTCCAGGGGAGGCTGCGCACTTGTGGCAAGTACCTCTTC 7560
7561 AACTGGGAGTAAGCAACAGCTCAAACTCACTCCAAATCCCGGCTGGCTCCAGTTGAT 7620
7561 AACTGGGAGTAAGCAACAGCTCAAACTCACTCCAAATCCCGGCTGGCTCCAGTTGAT 7620
7621 TTATCCAGTGGTTCGTTCTGCTGTTACAGCGGGGAGACATATACAGACCTGCTCTGT 7680
7621 TTATCCAGTGGTTCGTTCTGCTGTTACAGCGGGGAGACATATACAGACCTGCTCTGT 7680
7681 GCCGACCCGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7740
7681 GCCGACCCGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7740
7741 CTACTCCCCAACGATGAAGCGGAGCTAAACTCCAGGCGAATAGGCACTCTTTT 7800
7741 CTACTCCCCAACGATGAAGCGGAGCTAAACTCCAGGCGAATAGGCACTCTTTT 7800
7801 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
7801 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
7861 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
7861 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
7921 TAGCTGTGAAGGTCGCTGAGCGCTGATCTGATGAGAGTCTGATGAGTCTGCTCTGC 7980
7921 TAGCTGTGAAGGTCGCTGAGCGCTGATCTGATGAGAGTCTGATGAGTCTGCTCTGC 7980
7981 AGATCAAGTACT 7992

||||| 7981 AGATCAAGTACT 7992
RESULT 5
AAL47281
ID AAL47281 standard; DNA; 7992 BP.
XX
AC AAL47281;
XX 30-AUG-2002 (first entry)
XX Hepatitis C virus sub-genomic replicon recombinant clone HCV24.
XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
KW virucide; hepatotropic; gene therapy; anti-viral; gene; ds.
XX Hepatitis C virus.
OS
PN W0200238793-A2.
XX
PD 16-MAY-2002.
XX
XX 02-NOV-2001; 2001WO-US046350.
PF
XX 07-NOV-2000; 2000US-0245866P.
PR
XX
PA (ANAD-) ANADYS PHARM INC.
XX Bichko V;
XX WPI; 2002-490082/52.
DR
XX
XX Novel nucleic acid encoding replication competent recombinant hepatitis C
virus genome useful for screening anti-hepatitis C virus therapeutics and
for vaccine development.
Claim 11; Page 70-75; 85pp; English.
The present invention provides protein and coding sequences from
Hepatitis C virus (HCV), comprising all or part of the HCV genome and
able to replicate efficiently when transfected into a susceptible cell
line without reducing the growth rate of the cell line by more than 10
fold. The sequences are useful for screening for anti-HCV therapeutics,
for detecting antibodies to HCV in a biological sample such as blood,
serum, plasma, blood cells, lymphocytes, or liver cells from a subject.
for deriving authentic HCV components such as replication-competent non-
infectious, replication-defective infection-component, and replication-
defective non-infectious HCV, in gene therapy or gene vaccination
targeted to hepatic tissue for treating an animal infected or susceptible
to HCV infection and for studying HCV infection and propagation. The
present sequence is a clone of a fragment of the HCV genome designated
HCV24
XX Sequence 7992 BP; 1648 A; 2369 C; 2242 G; 1733 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 7990.4; DB 6; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAGCCCCGATTTGGGGCGACACCTCCACCATAGATCACTCCCTGTGAGGAATCTG 60
Db 1 GCCAGCCCCGATTTGGGGCGACACCTCCACCATAGATCACTCCCTGTGAGGAATCTG 60
QY 61 TCTTCCAGCAGAAAGCGTCTAGCCATGGCTTAGTATGAGTGTGTCGACCTCCAGGAC 120
Db 61 TCTTCCAGCAGAAAGCGTCTAGCCATGGCTTAGTATGAGTGTGTCGACCTCCAGGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAACCGGTGAGTACACCCGGAATTCAG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAACCGGTGAGTACACCCGGAATTCAG 180
QY 181 GACGACCGGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGCGCTGCC 240

181 GACACGGGTCTTCTTCTGATCAACCCCGTCAATGCTGGAGATTGGCGGTGCCCC 240
241 GCGAGACTGTAGCGAGTAGTGTGGGTGCGAAAGCCCTTGTGTACTGCTGTATAGG 300
241 GCGAGACTGTAGCGAGTAGTGTGGGTGCGAAAGCCCTTGTGTACTGCTGTATAGG 300
301 GTGCTTGCGAGTCCCGCGGAGGTCTCGTAGACGTGTGACATGAGCAAGATCTTAAAC 360
301 GTGCTTGCGAGTCCCGCGGAGGTCTCGTAGACGTGTGACATGAGCAAGATCTTAAAC 360
361 CTCAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATTTGTCAGAGTTCTC 420
361 CTCAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATTTGTCAGAGTTCTC 420
421 CGGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACACAGACAATCGGCTGT 480
421 CGGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACACAGACAATCGGCTGT 480
481 CTGATGCCCGCTGTTCGGCTGTGAGCGAGGGGCGCGGTTCTTTTGTCAAGACCG 540
481 CTGATGCCCGCTGTTCGGCTGTGAGCGAGGGGCGCGGTTCTTTTGTCAAGACCG 540
541 ACCTGTCCGGTCCCTGATGAATGACAGAGCGAGCGCGGCTATCGTGGCTGGCA 600
541 ACCTGTCCGGTCCCTGATGAATGACAGAGCGAGCGCGGCTATCGTGGCTGGCA 600
601 CGAGCGGCGTTCCTTGGCGAGCTGTGCTGAGCTGTCACTGAAGCGGAGGAGTGGC 660
601 CGAGCGGCGTTCCTTGGCGAGCTGTGCTGAGCTGTCACTGAAGCGGAGGAGTGGC 660
661 TGCTATTGGGCGAGTGCAGGCGAGGATCTCTGTGATCTCACTTGTCACTGGCGGAG 720
661 TGCTATTGGGCGAGTGCAGGCGAGGATCTCTGTGATCTCACTTGTCACTGGCGGAG 720
721 AAGTATCCATCATGGCTGATCAATGCGCGGCTGCTATACCTGTCTCTGCGGAGA 780
721 AAGTATCCATCATGGCTGATCAATGCGCGGCTGCTATACCTGTCTCTGCGGAGA 780
781 CATTCGACCAACAGCGAAACATCGATCGAGCGAGCAGTCTCGGATGGAAGCGGTC 840
781 CATTCGACCAACAGCGAAACATCGATCGAGCGAGCAGTCTCGGATGGAAGCGGTC 840
841 TTGTGATCAGGATGATCGAGCAAGAGCATCAGGGGCTCGCGCCAGCGGAACTGTGC 900
841 TTGTGATCAGGATGATCGAGCAAGAGCATCAGGGGCTCGCGCCAGCGGAACTGTGC 900
901 CAGGCTCAAGGCGCGCATGCCGACGCGAGGATCTCGTGACCCATGGCGATGCT 960
901 CAGGCTCAAGGCGCGCATGCCGACGCGAGGATCTCGTGACCCATGGCGATGCT 960
961 GCTTGGCGAATCATGGTGGAAATGGCGCTTTCTGGATTCACTGACTGTGGCGGC 1020
961 GCTTGGCGAATCATGGTGGAAATGGCGCTTTCTGGATTCACTGACTGTGGCGGC 1020
1021 TGGGTGTGGCGGACGCTATCAGGACATAGCTGTGGTACCCGTGATATGCTGAAGAGC 1080
1021 TGGGTGTGGCGGACGCTATCAGGACATAGCTGTGGTACCCGTGATATGCTGAAGAGC 1080
1081 TTGGCGGCAATGGGCTGACCGCTTCTCTGTGCTTTACGATCGCGCTCCCGATTGCG 1140
1081 TTGGCGGCAATGGGCTGACCGCTTCTCTGTGCTTTACGATCGCGCTCCCGATTGCG 1140
1141 AGCGATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAAGC 1200
1141 AGCGATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAAGC 1200
1201 GTTTCCTCTAGCGGATCAATTCGCCCTCTCCCTCCCGCCCTTAACGTTACTGCG 1260
1201 GTTTCCTCTAGCGGATCAATTCGCCCTCTCCCTCCCGCCCTTAACGTTACTGCG 1260
1261 CGAAGCGCTTGGAAATGAAGCGGCTGTGGTGTGCTATGTTTATTTCCACCATATG 1320

1261 CGAAGCGCTTGGAAATGAAGCGGCTGTGGTGTGCTATATGTTATTTCCACCATATG 1320
1321 CGGCTTTTGGCAATGTAGGGCCCGGAAACCTTGGCCCTGCTTCTTGTAGAGCATTCCT 1380
1321 CGGCTTTTGGCAATGTAGGGCCCGGAAACCTTGGCCCTGCTTCTTGTAGAGCATTCCT 1380
1381 AGGGGTCTTTCCTCTCTCGCCAAAGGAATGCAAGGTCTGTGTAATGTGTAAGGAAGCA 1440
1381 AGGGGTCTTTCCTCTCTCGCCAAAGGAATGCAAGGTCTGTGTAATGTGTAAGGAAGCA 1440
1441 GTTCTCTCTGGAAGCTTCTTGAAGACAAACAACTGTGTAGCGACCTTTGCAAGGCGG 1500
1441 GTTCTCTCTGGAAGCTTCTTGAAGACAAACAACTGTGTAGCGACCTTTGCAAGGCGG 1500
1501 AACCCCCCACTTGGGACAGGTGCTCTCGGCGCAAAAGCCAGTGTATATAGATACCT 1560
1501 AACCCCCCACTTGGGACAGGTGCTCTCGGCGCAAAAGCCAGTGTATATAGATACCT 1560
1561 GCAAAAGGCGGCAACCCCGAGTGCACAGTGTGTGATAGTGTGGAAGAGTCAAA 1620
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1621 TGCTCTCTCTCAAGCGTATTCAACAAAGGCGTGAAGATGCCAGAGTACCCATTGT 1680
1681 ATGGATCTGATCTGGGCGCTCGGTGCACATGCTTACATGTGTGTAGTTCGAGGTTAAA 1740
1681 ATGGATCTGATCTGGGCGCTCGGTGCACATGCTTACATGTGTGTAGTTCGAGGTTAAA 1740
1741 AACGTCTAGGCGGCGGCAACCCCGAGTGCACAGTGTGTGGAAGAGTCAAA 1800
1741 AACGTCTAGGCGGCGGCAACCCCGAGTGCACAGTGTGTGGAAGAGTCAAA 1800
1801 ATGGCGCTATTACGGCTACTTCCCAACAGACGCGAGGCTTACTTGGCTGATCATCACT 1860
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1861 AGCTCTACAGCGCGGACAGGAACAGGTCTGAGGGGAGGTCCAAAGTCTCCACCGCA 1920
1861 AGCTCTACAGCGCGGACAGGAACAGGTCTGAGGGGAGGTCCAAAGTCTCCACCGCA 1920
1921 ACACAACTTCTTCTGCGGACCTGCGTCAATGGCGTGTGTGGAAGTCTATCATGTTGCC 1980
1921 ACACAACTTCTTCTGCGGACCTGCGTCAATGGCGTGTGTGGAAGTCTATCATGTTGCC 1980
1981 GGCTCAAAAGACCTTGGCGGCGGCAAGGCGGCTTCCCTTGAACCAATGTACCAATGTGAC 2040
1981 GGCTCAAAAGACCTTGGCGGCGGCAAGGCGGCTTCCCTTGAACCAATGTACCAATGTGAC 2040
2041 CAGGACTCTGCTGGCTGGCAAGCGGCGGCTTCCCTTGAACCAATGTACCAATGTGAC 2100
2041 CAGGACTCTGCTGGCTGGCAAGCGGCGGCTTCCCTTGAACCAATGTACCAATGTGAC 2100
2101 GGCAGCTCGGACCTTTACTTGTGTGATGAGGATGCGGATGCGGCTGCGGCGG 2160
2101 GGCAGCTCGGACCTTTACTTGTGTGATGAGGATGCGGATGCGGCTGCGGCGG 2160
2161 GGCAGCAGCAGGCGGAGCTTCTTCCCGGCGGCTTCTTCTGAGGCTTCTTCCG 2220
2161 GGCAGCAGCAGGCGGAGCTTCTTCCCGGCGGCTTCTTCTGAGGCTTCTTCCG 2220
2221 GGCAGTCTGCTTGGCGGCAAGGCGGCTTGTGAGGCTTGTACCGCTGAGTATGAAACCACTATG 2280
2221 GGCAGTCTGCTTGGCGGCAAGGCGGCTTGTGAGGCTTGTACCGCTGAGTATGAAACCACTATG 2280
2281 ACCCGAGGGTGTGGAAGGCGGCTTGTGAGGCTTGTACCGCTGAGTATGAAACCACTATG 2340
2281 ACCCGAGGGTGTGGAAGGCGGCTTGTGAGGCTTGTACCGCTGAGTATGAAACCACTATG 2340
2341 CGGTCGCGGCTTTCACCGCAACTGCTCCCTCCGCGGTACCGGAGATTCAGGCTG 2400
2341 CGGTCGCGGCTTTCACCGCAACTGCTCCCTCCGCGGTACCGGAGATTCAGGCTG 2400

QY	2401	GCCCATCTACAGGCCCTTACTGTGTAGCGGCAAGACACTAAGGTGCGGCTGCGTATGCA	2460
DB	2401	GCCCATCTACAGGCCCTTACTGTGTAGCGGCAAGACACTAAGGTGCGGCTGCGTATGCA	2460
QY	2461	GCCCAAGGGTAAAGGTGCTTGTCTGTAACCCGTCGTCGCCGCCACCCCTAGTTTCGGG	2520
DB	2461	GCCCAAGGGTAAAGGTGCTTGTCTGTAACCCGTCGTCGCCGCCACCCCTAGTTTCGGG	2520
QY	2521	GGGTATATGCTTAAGGCACATGGTATCGACCTAATCATCAGAACCGGGTAAAGACCATC	2580
DB	2521	GGGTATATGCTTAAGGCACATGGTATCGACCTAATCATCAGAACCGGGTAAAGACCATC	2580
QY	2581	ACCACGGTGCCCCCATACAGTACTCCACTATGCAAGTTTCTTCCGACCGTGGTTGC	2640
DB	2581	ACCACGGTGCCCCCATACAGTACTCCACTATGCAAGTTTCTTCCGACCGTGGTTGC	2640
QY	2641	TCTGGGGCGCCTATCAGACATCAATATGTGATGAGTGCACCTCAATGACTCGACCAT	2700
DB	2641	TCTGGGGCGCCTATCAGACATCAATATGTGATGAGTGCACCTCAATGACTCGACCAT	2700
QY	2701	ATCCTGGGCATCGGCACAGTCTGGACAAAGCGGAGACGGCTGGAGGCGACTCGTCGTG	2760
DB	2701	ATCCTGGGCATCGGCACAGTCTGGACAAAGCGGAGACGGCTGGAGGCGACTCGTCGTG	2760
QY	2761	CTCGCCACCGCTAGCCCTCGGGATCGGTACCGTCCACGTGCCACATCCAAACATCGAGGAGGTG	2820
DB	2761	CTCGCCACCGCTAGCCCTCGGGATCGGTACCGTCCACGTGCCACATCCAAACATCGAGGAGGTG	2820
QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCCCTTTTATGGCAAGGCCATCCCATCGAGACCATC	2880
DB	2821	GCTCTGTCCAGCACTGGAGAAATCCCCCTTTTATGGCAAGGCCATCCCATCGAGACCATC	2880
QY	2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATCGATGAGCTCGCCGCG	2940
DB	2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATCGATGAGCTCGCCGCG	2940
QY	2941	AAGTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACCGGGGCTTGATGTATCGTTC	3000
DB	2941	AAGTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACCGGGGCTTGATGTATCGTTC	3000
QY	3001	ATACCAACTAGCGGAGACGTCAATGCTGTAGCAACGGACGGTCTAATGACGGGCTTTACC	3060
DB	3001	ATACCAACTAGCGGAGACGTCAATGCTGTAGCAACGGACGGTCTAATGACGGGCTTTACC	3060
QY	3061	GGCGATTTTCCGATAGTGTGATGACGTGCAATATGCTGTACATGTGTACCGACAGTCCGACTTCAGC	3120
DB	3061	GGCGATTTTCCGATAGTGTGATGACGTGCAATATGCTGTACATGTGTACCGACAGTCCGACTTCAGC	3120
QY	3121	CTGGACCGGACCTTACCACTTGGAGACGACCGTCCCAAGACGGCGTGTCAAGCTCG	3180
DB	3121	CTGGACCGGACCTTACCACTTGGAGACGACCGTCCCAAGACGGCGTGTCAAGCTCG	3180
QY	3181	CAGCGCGGAGGAGGACTGGTATGGGCGAGGATGGGCAATTTACAGTTTGTGACTCCAGCA	3240
DB	3181	CAGCGCGGAGGAGGACTGGTATGGGCGAGGATGGGCAATTTACAGTTTGTGACTCCAGCA	3240
QY	3241	GAAACGGCCCTCGGGCATGTTGATTTCTCGTGTGCGAGTGTATGACGGGCGCTGT	3300
DB	3241	GAAACGGCCCTCGGGCATGTTGATTTCTCGTGTGCGAGTGTATGACGGGCGCTGT	3300
QY	3301	GCTTGTGTACGAGCTCACGCCCGCGAGACCTCAGTTAGTTTGGGGGCTTACCTAAACACA	3360
DB	3301	GCTTGTGTACGAGCTCACGCCCGCGAGACCTCAGTTAGTTTGGGGGCTTACCTAAACACA	3360
QY	3361	CCAGGGTTGCCCGTCTGCCAGGACCATCTGGAGTCTTGGAGAGCGCTTTTACAGGCGCTC	3420
DB	3361	CCAGGGTTGCCCGTCTGCCAGGACCATCTGGAGTCTTGGAGAGCGCTTTTACAGGCGCTC	3420
QY	3421	ACCCACATAGACGCGCAATTTCTTCCAGACTAAGCAGCAGGAGACAACTTCCCCCTAC	3480
DB	3421	ACCCACATAGACGCGCAATTTCTTCCAGACTAAGCAGCAGGAGACAACTTCCCCCTAC	3480

QY	3481	CTGTAGCATACACAGGCTACGGTGTGGCCACAGGCTCAGGCTCCACTCTCCATCGTGGGAC	3540
DB	3481		
QY	3481	CTGTAGCATACCAAGGCTACGGTGTGGCCAGGCTCAGGCTCCACTCGTGGGAC	3540
DB	3481		
QY	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCACGGCCAAACGCCCTGTGTG	3600
DB	3541	CAAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCACGGCCAAACGCCCTGTGTG	3600
QY	3601	TATAGCTGGGAGCCGTTCAAACACGAGTTACTACACACACCCATAACCAATACATC	3660
DB	3601	TATAGCTGGGAGCCGTTCAAACACGAGTTACTACACACACCCATAACCAATACATC	3660
QY	3661	ATGGCATGCACTCTCGCTGACCTGGAGTGTGTCAAGACACCTGGTGTGTGTAGCGGA	3720
DB	3661	ATGGCATGCACTCTCGCTGACCTGGAGTGTGTCAAGACACCTGGTGTGTGTAGCGGA	3720
QY	3721	GTCTTAGCAGCTCTGGCCCGTATTGCTGTGAACAGGACAGCTGTGTCAATGTGGGCGAG	3780
DB	3721	GTCTTAGCAGCTCTGGCCCGTATTGCTGTGAACAGGACAGCTGTGTCAATGTGGGCGAG	3780
QY	3781	ATCACTCTGTCCGAAAGCGGCCATCTTCCGACAGGGAAGTCTTTACCGGGAGTTC	3840
DB	3781	ATCACTCTGTCCGAAAGCGGCCATCTTCCGACAGGGAAGTCTTTACCGGGAGTTC	3840
QY	3841	GATGAGATGGAAGTGGCCTCACACCTCCCTTACATCGAAACAGGGAATGCAGCTCGCC	3900
DB	3841	GATGAGATGGAAGTGGCCTCACACCTCCCTTACATCGAAACAGGGAATGCAGCTCGCC	3900
QY	3901	GAAACAATTTCAAACAGAAAGCAATCGGGTTGCTGAAACAGCCACCAAGCAGCGAGGCT	3960
DB	3901	GAAACAATTTCAAACAGAAAGCAATCGGGTTGCTGAAACAGCCACCAAGCAGCGAGGCT	3960
QY	3961	GCTGCTCCGCTGTGGAAATCCAAAGTGGCGGACCTCGAAGCTTCTGGGCGAAACATATG	4020
DB	3961	GCTGCTCCGCTGTGGAAATCCAAAGTGGCGGACCTCGAAGCTTCTGGGCGAAACATATG	4020
QY	4021	TGGAATTTCAATCAGCGGGATACAAATATTAGCAGGCTGTCCACTCTGCTGGCAACCC	4080
DB	4021	TGGAATTTCAATCAGCGGGATACAAATATTAGCAGGCTGTCCACTCTGCTGGCAACCC	4080
QY	4081	GCATAGCATCACTGATGGCATTCACAGCTCTATCACCAGCCGCTCACCACCCAAAT	4140
DB	4081	GCATAGCATCACTGATGGCATTCACAGCTCTATCACCAGCCGCTCACCACCCAAAT	4140
QY	4141	ACCTCTCGTTTACATCTCGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCT	4200
DB	4141	ACCTCTCGTTTACATCTCGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGCGCT	4200
QY	4201	GCTTCTGCTTTCGTAGGCGCCGCATCGCTGGAGCGCTGTGTGGCAGCATAGCCCTGGG	4260
DB	4201	GCTTCTGCTTTCGTAGGCGCCGCATCGCTGGAGCGCTGTGTGGCAGCATAGCCCTGGG	4260
QY	4261	AAGTGTCTGTGGATATTTTGGCAGGTTATGGACAGGGGTGGCAGCGCGTCTGTGGCC	4320
DB	4261	AAGTGTCTGTGGATATTTTGGCAGGTTATGGACAGGGGTGGCAGCGCGTCTGTGGCC	4320
QY	4321	TTTAAAGTTCATGAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTACTTCCCTGCT	4380
DB	4321	TTTAAAGTTCATGAGCGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTACTTCCCTGCT	4380
QY	4381	ATCCCTCTCCCTCGGGCCCTAGTCGTGGGGTGTGTGGCAGCGATATGCTGTGGCAC	4440
DB	4381	ATCCCTCTCCCTCGGGCCCTAGTCGTGGGGTGTGTGGCAGCGATATGCTGTGGCAC	4440
QY	4441	GTGGGCCACAGGGAGGGGCTGTGCAGTGAATGAAACCGGCTGATAGCTTTCGCTTCGCGG	4500
DB	4441	GTGGGCCACAGGGAGGGGCTGTGCAGTGAATGAAACCGGCTGATAGCTTTCGCTTCGCGG	4500
QY	4501	GGTAAACAGCTCTCCGCCACGCACTATGTGCCTGAGAGCGACGTGTGACACGTGTCACT	4560
DB	4501	GGTAAACAGCTCTCCGCCACGCACTATGTGCCTGAGAGCGACGTGTGACACGTGTCACT	4560
QY	4561	CAGATCCTCTCTAGTCTTACATCACTCAGCTGCTGAAGGGCTTCCACGATGGATCAAC	4620

QY	7861	TTTTTCTCTTTTTCCTTTTCTTTCTTTCTTTGGTGTCCATCTTAGCCCTTAGTCACGGC	7920
Db	7861	TTTTTCTCTTTTTCCTTTTCTTTCTTTCTTTGGTGTCCATCTTAGCCCTTAGTCACGGC	7920
QY	7921	TAGCTGTGAAGGTCCGTGAGCCGCTTGACTGCAGAGAGTGCTGATACTGGCCCTCTCTGC	7980
Db	7921	TAGCTGTGAAGGTCCGTGAGCCGCTTGACTGCAGAGAGTGCTGATACTGGCCCTCTCTGC	7980
QY	7981	AGATCAAGTACT 7992	
Db	7981	AGATCAAGTACT 7992	
RESULT 6			
ID	ABK91448	standard; DNA; 10690 BP.	
XX	AC	ABK91448;	
XX	DT	15-NOV-2002 (first entry)	
XX	DE	Hepatitis C virus vector construct pHCVNeo.17mi5.	
XX	XX	HCV; ss; pHCVNeo.17mi2; adaptive mutation; liver failure; cirrhosis;	
KW	KW	hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;	
KW	KW	internal ribosome entry site; IRES; NS5A; HCV replication; mutant.	
XX	OS	Hepatitis C virus.	
OS	OS	Encephalomyocarditis virus.	
OS	OS	Escherichia coli.	
OS	OS	Enterobacteria phage T7.	
OS	OS	Synthetic.	
XX	XX	Location/Qualifiers	
FH	FT	1..341	
FT	FT	5'UTR	
FT	FT	/*tag= a	
FT	FT	342..1181	
FT	FT	/*tag= b	
FT	FT	/product= "Core-neo fusion protein"	
FT	FT	1190..1800	
FT	FT	misc_signal	
FT	FT	/*tag= c	
FT	FT	/label= IRES	
FT	FT	/note= "Internal ribosome entry site from BCMV"	
FT	FT	1801..7758	
FT	FT	/*tag= d	
FT	FT	/product= "Polyprotein"	
FT	FT	/note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"	
FT	FT	replace(5320,G)	
FT	FT	/*tag= e	
FT	FT	7759..7991	
FT	FT	/*tag= f	
FT	FT	7992..10690	
FT	FT	misc_feature	
FT	FT	/*tag= g	
FT	FT	/note= "Plasmid derived sequences"	
XX	XX		
PN	XX	WO200259321-A2.	
XX	XX		
PD	XX	01-AUG-2002.	
XX	XX		
PF	XX	16-JAN-2002; 2002WO-EP000526.	
XX	XX		
PR	XX	23-JAN-2001; 2001US-0263479P.	
XX	XX	(RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.	
PA	XX		
PI	XX	De Francesco R, Migliaccio G, Paonessa G;	
XX	XX		
DR	XX	WPI; 2002-599793/64.	
XX	XX	New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV	
PT	PT	NS5 encoding region, or encephalomyocarditis virus (EMCV) internal	
PT	PT	ribosome entry site (IRES) region, useful in studying HCV replication ar	
PT	PT	expression.	

XX
PS
XX

Claim 16; Page; 69pp; English.

The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV based vector pHCVNeo.17 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV vector sequence appearing as ABK91412 and the information in Claim 16

Sequence 10690 BP; 2335 A; 3045 C; 2907 G; 2403 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 7990.4; DB 6; Length 10690;

Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GCCAGCCCCCGATTGGGGCGACACTCACACATAGATCACTCCCTGTGAGGAATCTACTG	60
DB	1	GCCAGCCCCCGATTGGGGCGACACTCACACATAGATCACTCCCTGTGAGGAATCTACTG	60
QY	61	TCTTCACGACAGAACGCTTAGCCATGCGTGTAGTATGAGTGTCTGAGCCTCCAGGAC	120
DB	61	TCTTCACGACAGAACGCTTAGCCATGCGTGTAGTATGAGTGTCTGAGCCTCCAGGAC	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGCGCAG	180
DB	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGCGCAG	180
QY	181	GACGACCGGTTCCTTCTTGATCAACCCGCTCAATGCTCGAGATTGGCGTGCCCC	240
DB	181	GACGACCGGTTCCTTCTTGATCAACCCGCTCAATGCTCGAGATTGGCGTGCCCC	240
QY	241	GCGAGACTGCTAGCCGAGTAGTGTGGTGTGCGAAGCGCTTGTGTTACTGCTGATAGG	300
DB	241	GCGAGACTGCTAGCCGAGTAGTGTGGTGTGCGAAGCGCTTGTGTTACTGCTGATAGG	300
QY	301	GTGCTTCGAGTGCCCGGAGGTCTCGTAGCCGTGCACCATGAGCAGCAATCCTAAAC	360
DB	301	GTGCTTCGAGTGCCCGGAGGTCTCGTAGCCGTGCACCATGAGCAGCAATCCTAAAC	360
QY	361	CTCAAGAAACAAAGGGCGGCCATGATGAAACAGATGAGTACGCGAGTTCTC	420
DB	361	CTCAAGAAACAAAGGGCGGCCATGATGAAACAGATGAGTACGCGAGTTCTC	420
QY	421	CGGCGCTTGGGTGGAGAGCTATTGCGCTATGACTGGGCAACAGCAATCGGTGCT	480
DB	421	CGGCGCTTGGGTGGAGAGCTATTGCGCTATGACTGGGCAACAGCAATCGGTGCT	480
QY	481	CTGATGCGCGGTGTTCCGCTGTACGCGAGGGCGCCGGTCTTTTGTCAAGACCG	540
DB	481	CTGATGCGCGGTGTTCCGCTGTACGCGAGGGCGCCGGTCTTTTGTCAAGACCG	540
QY	541	ACCTGTCCGCTGCGCTGAATGAACTGAGGACGAGCGCGGCTATCGTGGCTGGCCA	600
DB	541	ACCTGTCCGCTGCGCTGAATGAACTGAGGACGAGCGCGGCTATCGTGGCTGGCCA	600
QY	601	CGACGGCGGTTCCTTCGCGAGCTGTCTCGACGTGTCTACTGAAGCGGAGGACTGGC	660

Db 1681 ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTTATCATGTGTTAGTCGAGGTTAAAA 1740
Qy 1741 AACGTCCTAGGCCCCCGAACCACGCGGACGTGGTTTTCTTTTGAAGAAACACGATATATACC 1800
Db 1741 RACGTCCTAGGCCCCCGAACCACGCGGACGTGGTTTTCTTTTGAAGAAACACGATATATACC 1800
Qy 1801 ATGGGCGCTATTACGGCCTACTCCAAACAGACGCGAGGCTACTTGGCTGCAATCATCACT 1860
Db 1801 ATGGGCGCTATTACGGCCTACTCCAAACAGACGCGAGGCTACTTGGCTGCAATCATCACT 1860
Qy 1861 AGCCTCAGAGCGCGGACAGGACAGGTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
Db 1861 AGCCTCAGAGCGCGGACAGGACAGGTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
Qy 1921 ACACAACTTTCTGCGGACCTCGCTCAATGGCGTGTGTGGAGCTGTCTATCATGTGTC 1980
Db 1921 ACACAACTTTCTGCGGACCTCGCTCAATGGCGTGTGTGGAGCTGTCTATCATGTGTC 1980
Qy 1981 GGCTCAAGACCTTTGCGGCCCCAAGGGCCCCAATCACCAAAATGTACCAAAATGTGGAC 2040
Db 1981 GGCTCAAGACCTTTGCGGCCCCAAGGGCCCCAATCACCAAAATGTACCAAAATGTGGAC 2040
Qy 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGAACACCATGACCTGC 2100
Db 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGAACACCATGACCTGC 2100
Qy 2101 GGCAGCTCGGACCTTTACTTTGGTCAAGGATGCGGATGTCATTCCGGTGGCGCGCG 2160
Db 2101 GGCAGCTCGGACCTTTACTTTGGTCAAGGATGCGGATGTCATTCCGGTGGCGCGCG 2160
Qy 2161 GGCAGACGAGGGGAGGCTACTCTCCCGGCGGCTCTCTCTACTTTGAAGGGCTCTTCG 2220
Db 2161 GGCAGACGAGGGGAGGCTACTCTCCCGGCGGCTCTCTCTACTTTGAAGGGCTCTTCG 2220
Qy 2221 GGCAGCTCGGACCTTTACTTTGGTCAAGGATGCGGATGTCATTCCGGTGGCGCGCG 2280
Db 2221 GGCAGCTCGGACCTTTACTTTGGTCAAGGATGCGGATGTCATTCCGGTGGCGCGCG 2280
Qy 2281 ACCGAGGGGTGCGAAGGGGTGGAATTTGTATCCGTCGAGTCTATGGAACCACTATG 2340
Db 2281 ACCGAGGGGTGCGAAGGGGTGGAATTTGTATCCGTCGAGTCTATGGAACCACTATG 2340
Qy 2341 CGGTCCCGGTCTTACAGGCAACTCTGTCCTCCCGGCGGTACCGAGACATTTCCAGGTG 2400
Db 2341 CGGTCCCGGTCTTACAGGCAACTCTGTCCTCCCGGCGGTACCGAGACATTTCCAGGTG 2400
Qy 2401 GCGCATCTACGCGCCCTACTGTTAGCGGCAAGAGCACTAAGGTCCCGGTGCGTATGCA 2460
Db 2401 GCGCATCTACGCGCCCTACTGTTAGCGGCAAGAGCACTAAGGTCCCGGTGCGTATGCA 2460
Qy 2461 GCGCAAGGGTATAGGTGTTGTCCTGAAACCGGTCCGTCGCGGCGGACCTAGGTTTCGG 2520
Db 2461 GCGCAAGGGTATAGGTGTTGTCCTGAAACCGGTCCGTCGCGGCGGACCTAGGTTTCGG 2520
Qy 2521 GGGTATATCTTAAGGCATCATGATTCGACCTTAATCATAGAACCGGGTAAAGCACTC 2580
Db 2521 GGGTATATCTTAAGGCATCATGATTCGACCTTAATCATAGAACCGGGTAAAGCACTC 2580
Qy 2581 ACCACGGGTGCCCCCATACGTAATCCACTATGGAAGTTCCTGCGAGCGGTGTTGC 2640
Db 2581 ACCACGGGTGCCCCCATACGTAATCCACTATGGAAGTTCCTGCGAGCGGTGTTGC 2640
Qy 2641 TCTGGGGGCGCTATGACATCATATATGATGAGTGGCCACTCACTGACCTGACCACT 2700
Db 2641 TCTGGGGGCGCTATGACATCATATATGATGAGTGGCCACTCACTGACCTGACCACT 2700
Qy 2701 ATCTTGGGATCGGACAGTCTTGAACAGCGGAGACGGCTGGAGCGGACCTCGTCGTG 2760
Db 2701 ATCTTGGGATCGGACAGTCTTGAACAGCGGAGACGGCTGGAGCGGACCTCGTCGTG 2760
Qy 2761 CTGCGCACCGCTAGCGCTCCGGGATCGGTCAACCGTGCACATCCAAACATCGAGGAGTG 2820
Db 2761 CTGCGCACCGCTAGCGCTCCGGGATCGGTCAACCGTGCACATCCAAACATCGAGGAGTG 2820

Qy 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGCCATCCCATCGAGACCATC 2880
Db 2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGCCATCCCATCGAGACCATC 2880
Qy 2881 AAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATGTGATGAGCTCGCGG 2940
Db 2881 AAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATGTGATGAGCTCGCGG 2940
Qy 2941 AAGCTGTCCGGCTCGGACTCAATGCTGATGATATTTACCGGGGCTTCAATGATCCGTC 3000
Db 2941 AAGCTGTCCGGCTCGGACTCAATGCTGATGATATTTACCGGGGCTTCAATGATCCGTC 3000
Qy 3001 ATACCAACTAGCGGAGACGTATTTGTGTAGCAACGAGCGCTTAATGACGGGCTTTACC 3060
Db 3001 ATACCAACTAGCGGAGACGTATTTGTGTAGCAACGAGCGCTTAATGACGGGCTTTACC 3060
Qy 3061 GGGATTTTCGACTCAGTGATCGACTCAATGCTGATGATATTTACCGGGGCTTCAATGATCCGTC 3120
Db 3061 GGGATTTTCGACTCAGTGATCGACTCAATGCTGATGATATTTACCGGGGCTTCAATGATCCGTC 3120
Qy 3121 CTGGACCCGACCTTCAACATTTGAGACGACGACCGTGCACAGCGGGTGTACGCTCG 3180
Db 3121 CTGGACCCGACCTTCAACATTTGAGACGACGACCGTGCACAGCGGGTGTACGCTCG 3180
Qy 3181 CAGCGGGGAGGACGACTGTTAGGGCAGGATGGCATTTTACAGGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGGGAGGACGACTGTTAGGGCAGGATGGCATTTTACAGGTTTGTGACTCCAGGA 3240
Qy 3241 GAACGGCTCTCGGCACTGTTTCGATTTCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT 3300
Db 3241 GAACGGCTCTCGGCACTGTTTCGATTTCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT 3300
Qy 3301 GCTTGTGTACGAGCTCAGCGCGCGGACGACCTCAGTTAGTTTGGGGCTTACCTAAACACA 3360
Db 3301 GCTTGTGTACGAGCTCAGCGCGCGGACGACCTCAGTTAGTTTGGGGCTTACCTAAACACA 3360
Qy 3361 CAGGGTTGCCGCTCTCGGAGCACCTGAGTTCTGGGAGAGCTCTTTTACAGGCGCTC 3420
Db 3361 CAGGGTTGCCGCTCTCGGAGCACCTGAGTTCTGGGAGAGCTCTTTTACAGGCGCTC 3420
Qy 3421 ACCCACATAGACGCCCTTTCTTCTCCAGACTAAGCAGGAGGAGAGCAATTTCCCTTAC 3480
Db 3421 ACCCACATAGACGCCCTTTCTTCTCCAGACTAAGCAGGAGGAGAGCAATTTCCCTTAC 3480
Qy 3481 CTGGTAGCATACAGGCTACGGTGTGCGGACGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Db 3481 CTGGTAGCATACAGGCTACGGTGTGCGGACGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Qy 3541 CAATGTGGAGTGTCTCATACGGTAAAGCTACGTCGACGGGCGCAACGCCCTGTGTG 3600
Db 3541 CAATGTGGAGTGTCTCATACGGTAAAGCTACGTCGACGGGCGCAACGCCCTGTGTG 3600
Qy 3601 TATAGCTGGGAGCGGTTCAAAACGAGGTTTACTACACACACCCCATTAACCAATACATC 3660
Db 3601 TATAGCTGGGAGCGGTTCAAAACGAGGTTTACTACACACACCCCATTAACCAATACATC 3660
Qy 3661 ATGGCATGATGCTGCGTACCTGAGGTCGTACAGGACCTGGGTGCTGTAGCGGA 3720
Db 3661 ATGGCATGATGCTGCGTACCTGAGGTCGTACAGGACCTGGGTGCTGTAGCGGA 3720
Qy 3721 GTCTTAGAGCTCTGGCGCGGTATTTGCTGACAAAGGAGGAGGCTGATTTGTGGGACG 3780
Db 3721 GTCTTAGAGCTCTGGCGCGGTATTTGCTGACAAAGGAGGAGGCTGATTTGTGGGACG 3780
Qy 3781 ATCATCTTCTCGGAAAGCGGCGCATTTTCCCGACAGGAAAGTCTTTTACCGGGAGTTC 3840
Db 3781 ATCATCTTCTCGGAAAGCGGCGCATTTTCCCGACAGGAAAGTCTTTTACCGGGAGTTC 3840
Qy 3841 GATGAGATGGAAGTGGCGCTCACACCTCCCTTATCATCGAACAGGAAATGACGCTGCC 3900
Db 3841 GATGAGATGGAAGTGGCGCTCACACCTCCCTTATCATCGAACAGGAAATGACGCTGCC 3900

QY	3901	GAACAATTCAAAACAGAAAGCAATTCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGAGGCT	3960
Db	3901	GAACAATTCAAAACAGAAAGCAATTCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGAGGCT	3960
QY	3961	GCTGCTCCGGTGGTGGAAATCCAAGTGGCGGACCCCTCGAAGCCCTTCTGGGCGAAGCATATG	4020
Db	3961	GCTGCTCCGGTGGTGGAAATCCAAGTGGCGGACCCCTCGAAGCCCTTCTGGGCGAAGCATATG	4020
QY	4021	TGGAATTTTCATCAGCGGGGATACAAATATTTAGCAGGCTTGTCCACTCTGCTGCCAACC	4080
Db	4021	TGGAATTTTCATCAGCGGGGATACAAATATTTAGCAGGCTTGTCCACTCTGCTGCCAACC	4080
QY	4081	CGATAGCATCACTGATGCAATTCACAGCCTCTATCACAGCCCGCTCACACCCCAACAT	4140
Db	4081	CGATAGCATCACTGATGCAATTCACAGCCTCTATCACAGCCCGCTCACACCCCAACAT	4140
QY	4141	ACCTTCCTGTTTAAACATCCTGGGGGATGGGTGGCGCCCACTGCTCTCCACGCGT	4200
Db	4141	ACCTTCCTGTTTAAACATCCTGGGGGATGGGTGGCGCCCACTGCTCTCCACGCGT	4200
QY	4201	GCTTCTGCTTCTGAGGCGCGGCATCGCTGAGCGGCTGTGGCAGCATAGAGCCTTTGGG	4260
Db	4201	GCTTCTGCTTCTGAGGCGCGGCATCGCTGAGCGGCTGTGGCAGCATAGAGCCTTTGGG	4260
QY	4261	AAGTGTCTTGGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGCGC	4320
Db	4261	AAGTGTCTTGGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGCGC	4320
QY	4321	TTTAAAGTCAATGACGGCGAGATGCCCTCCACGAGGACCTGGTTAACTACTCCCTGCT	4380
Db	4321	TTTAAAGTCAATGACGGCGAGATGCCCTCCACGAGGACCTGGTTAACTACTCCCTGCT	4380
QY	4381	ATCCTCTCCCTCGCGCCCTAGTCTGGGGTCTGTGCGCAGCGATCTGGTGGGAC	4440
Db	4381	ATCCTCTCCCTCGCGCCCTAGTCTGGGGTCTGTGCGCAGCGATCTGGTGGGAC	4440
QY	4441	GTGGGCCCAGGGAGGGGGCTGTGATGATGAACCGGCTGTAGCGTTCCGTTCCGCGG	4500
Db	4441	GTGGGCCCAGGGAGGGGGCTGTGATGATGAACCGGCTGTAGCGTTCCGTTCCGCGG	4500
QY	4501	GGTAAACACGCTCTCCCCACGCACTATGCTGAGAGGCTTACCGGCTGATAGCGTTCCGTTCCGCGG	4560
Db	4501	GGTAAACACGCTCTCCCCACGCACTATGCTGAGAGGCTTACCGGCTGATAGCGTTCCGTTCCGCGG	4560
QY	4561	CAGATCCTCTAGTCTTACCATCACTCAGCTGCTGAAGGCTTACCGGCTGATAGCGTTCCGTTCCGCGG	4620
Db	4561	CAGATCCTCTAGTCTTACCATCACTCAGCTGCTGAAGGCTTACCGGCTGATAGCGTTCCGTTCCGCGG	4620
QY	4621	GAGGACTGCTCCACGCGATGCTCGGCTGTGAGAGGCTTACCGGCTGATAGCGTTCCGTTCCGCGG	4680
Db	4621	GAGGACTGCTCCACGCGATGCTCGGCTGTGAGAGGCTTACCGGCTGATAGCGTTCCGTTCCGCGG	4680
QY	4681	ACGGTGTGACTGATTTCAAGACCTCGCTCCAGTCCAGCTCCGCGGATTCGCGGATTCGCGGGA	4740
Db	4681	ACGGTGTGACTGATTTCAAGACCTCGCTCCAGTCCAGCTCCGCGGATTCGCGGATTCGCGGGA	4740
QY	4741	GTCCCTTCTTCTCATGTCAAAGTGGGTACAGGGAGTCTGGCGGGCGGCGGCGATCATG	4800
Db	4741	GTCCCTTCTTCTCATGTCAAAGTGGGTACAGGGAGTCTGGCGGGCGGCGGCGATCATG	4800
QY	4801	CAAAACCATCGCCATGTGAGCAGCATGCGGACATGTGAAAAACGGTTCCATGAGG	4860
Db	4801	CAAAACCATCGCCATGTGAGCAGCATGCGGACATGTGAAAAACGGTTCCATGAGG	4860
QY	4861	ATCGTGGGCGCTAGGACCTGTAGTAACAGTGGCATGGAACATTCCCATTTAACGGGTAC	4920
Db	4861	ATCGTGGGCGCTAGGACCTGTAGTAACAGTGGCATGGAACATTCCCATTTAACGGGTAC	4920
QY	4921	ACCAAGGCGCGCTGACGCGCTTCCCGCGCCAAATTTTCTAGGCGCTGTGGCGGGTG	4980
Db	4921	ACCAAGGCGCGCTGACGCGCTTCCCGCGCCAAATTTTCTAGGCGCTGTGGCGGGTG	4980
QY	4981	GCTGCTGAGGAGTACGTGGAGGTTACGCGGTGGGGATTTTCCATGATGACGGGCATG	5040

Db	4981	GCTGCTGAGGATACGTGTGAGGTTACGCGGTGGGGATTTCACACTACGTGACGGGATG	5040
Qy	5041	ACCACTGACAACGTAAGTGCCTGTGTAGGTTCCGGCCCCCGAAATCTTTACAGAAAGTG	5100
Db	5041	ACCACTGACAACGTAAGTGCCTGTGTAGGTTCCGGCCCCCGAAATCTTTACAGAAAGTG	5100
Qy	5101	GATGGGTGCGGTTCGCACAGGTACGCTCCAGCGTGCACAAACCCCTCTACGGGAGGAGTGC	5160
Db	5101	GATGGGTGCGGTTCGCACAGGTACGCTCCAGCGTGCACAAACCCCTCTACGGGAGGAGTGC	5160
Qy	5161	ACATTCCTGTGCGGCTCAATCAATACCTGTGGGTACAGCTCCCATTCGAGCCCGAA	5220
Db	5161	ACATTCCTGTGCGGCTCAATCAATACCTGTGGGTACAGCTCCCATTCGAGCCCGAA	5220
Qy	5221	CCGAGCGTAGCAGTGCTCACTTCATGTCAACGACCCCTCCCAATTCACGGCGAGACG	5280
Db	5221	CCGAGCGTAGCAGTGCTCACTTCATGTCAACGACCCCTCCCAATTCACGGCGAGACG	5280
Qy	5281	GCTAAGCGTAGGCTGGCCAGCGGATCTCCCGCTCTTGGCCAGCTCATCAGTAGCCAG	5340
Db	5281	GCTAAGCGTAGGCTGGCCAGCGGATCTCCCGCTCTTGGCCAGCTCATCAGTAGCCAG	5340
Qy	5341	CTGTCTCGCCTTCCCTTTGAAGCCAACTGCACTACCCGTCTATGATCCCGCGACGCTGAC	5400
Db	5341	CTGTCTCGCCTTCCCTTTGAAGCCAACTGCACTACCCGTCTATGATCCCGCGACGCTGAC	5400
Qy	5401	CTCATCGAGGCCAACCTCTGTGTGGCGCAGAGATGGCGGGAAATCAACCCGCTGGAG	5460
Db	5401	CTCATCGAGGCCAACCTCTGTGTGGCGCAGAGATGGCGGGAAATCAACCCGCTGGAG	5460
Qy	5461	TCAGAAATAAAGTGTAGTAATTTTGGACTCTTTGAGCGCGTCCAAAGCGGAGGAGTACG	5520
Db	5461	TCAGAAATAAAGTGTAGTAATTTTGGACTCTTTGAGCGCGTCCAAAGCGGAGGAGTACG	5520
Qy	5521	AGGGAAGTATCCGTTCCGGCGGAGATCCTCGGAGGTCCTAGGAAATTCCTTCGAGCGATG	5580
Db	5521	AGGGAAGTATCCGTTCCGGCGGAGATCCTCGGAGGTCCTAGGAAATTCCTTCGAGCGATG	5580
Qy	5581	CCCATATGGCAGCCCGGATTACAACCCCTCCACTGTTAGAGTCCCTGGAAGGACCCGGAC	5640
Db	5581	CCCATATGGCAGCCCGGATTACAACCCCTCCACTGTTAGAGTCCCTGGAAGGACCCGGAC	5640
Qy	5641	TAGCTCCCTCCAGTGTGTACACGGGTGCATTCGCGCTGCCAAGGCCCTCCGATACCA	5700
Db	5641	TAGCTCCCTCCAGTGTGTACACGGGTGCATTCGCGCTGCCAAGGCCCTCCGATACCA	5700
Qy	5701	CTTCCACGAGGAAGGAGCGGTTGTCTGTACGAATCTACCGTGCTTCTGCTTGGCG	5760
Db	5701	CTTCCACGAGGAAGGAGCGGTTGTCTGTACGAATCTACCGTGCTTCTGCTTGGCG	5760
Qy	5761	GAGCTCGCCACAAAGACCTTCGCGAGCTCCGAATCGTCGCGCTGCACACGGGACCGGCA	5820
Db	5761	GAGCTCGCCACAAAGACCTTCGCGAGCTCCGAATCGTCGCGCTGCACACGGGACCGGCA	5820
Qy	5821	ACGGCTCTCTGACAGCCCTTCGACACGGCAGCGGGATCCGATCTCAGCGACGGGTCTGG	5880
Db	5821	ACGGCTCTCTGACAGCCCTTCGACACGGCAGCGGGATCCGATCTCAGCGACGGGTCTGG	5880
Qy	5881	TCCTTCATGCCCCCTTTGAGGGGAGCCGGGGATCCGATCTCAGCGACGGGTCTTGG	5940
Db	5881	TCCTTCATGCCCCCTTTGAGGGGAGCCGGGGATCCGATCTCAGCGACGGGTCTTGG	5940
Qy	5941	TCTACCGTAAAGCGAGGAGCTAGTGAGGACGTCTGCTGCTCGATGTCCTTACATGG	6000
Db	5941	TCTACCGTAAAGCGAGGAGCTAGTGAGGACGTCTGCTGCTCGATGTCCTTACATGG	6000
Qy	6001	ACAGGCCCTGATCAAGCCATGGCTCGGAGGAAACCAAGCTGCCATCAATGCACTG	6060
Db	6001	ACAGGCCCTGATCAAGCCATGGCTCGGAGGAAACCAAGCTGCCATCAATGCACTG	6060
Qy	6061	AGCAACTCTTTGCTCCGCTCACCACAACTTGTGTATGCTACAACATCTCGACGCGAAGC	6120
Db	6061	AGCAACTCTTTGCTCCGCTCACCACAACTTGTGTATGCTACAACATCTCGACGCGAAGC	6120

6061 AGCAACTCTTTGCTCCGTCACCAACAATTGGTCTATGCTACCAATCTCGAGCGCAAGC 6120
 6121 CTGGGCGAAGAAAGGTCACTTTGACAGATGCGAGTCTCGAGCACCACTACCGGAC 6180
 6121 CTGGGCGAAGAAAGGTCACTTTGACAGATGCGAGTCTCGAGCACCACTACCGGAC 6180
 6181 GTGCTCAAGGAGATGAAGCGAAGCGTCCACAGTTAGGCTAAATCTCTATCCGTTGGAG 6240
 6181 GTGCTCAAGGAGATGAAGCGAAGCGTCCACAGTTAGGCTAAATCTCTATCCGTTGGAG 6240
 6241 GAAGCTGTAGCTGACGCCCCCAATTCCGGCAGATCTAAATTTGGCTATGGGCAAG 6300
 6241 GAAGCTGTAGCTGACGCCCCCAATTCCGGCAGATCTAAATTTGGCTATGGGCAAG 6300
 6301 GACGTCGGGAACTATCCAGCAAGCGGTAAACCAATCCGCTCCGTTGGAGAGACTTG 6360
 6301 GACGTCGGGAACTATCCAGCAAGCGGTAAACCAATCCGCTCCGTTGGAGAGACTTG 6360
 6361 CTGGAGACACTGAGACACCAATTGACACCACTATGCGTAAATGAGGTTTCTGTC 6420
 6361 CTGGAGACACTGAGACACCAATTGACACCACTATGCGTAAATGAGGTTTCTGTC 6420
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RESULT 7

ABK91435
 ID ABK91435 standard; DNA; 10690 BP.
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 AC ABK91435;
 XX
 DT 15-NOV-2002 (first entry)
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 DE Hepatitis C virus vector construct pHCVNeo.17m2.
 XX
 KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
 KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
 KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
 XX
 OS Hepatitis C virus.

OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.

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PN W0200259321-A2.

XX 01-AUG-2002.

PD 16-JAN-2002; 2002WO-EP0000526.

PF 23-JAN-2001; 2001US-0263479P.

PR (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.

PA De Francesco R, Magliaccio G, Paonessa G;

PI WPI; 2002-599793/64.

XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.

PS Claim 16; Page; 69pp; English.

CC The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replicons and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is an HCV based vector
CC pHCVneo.17 mutant of the invention. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the HCV
CC vector sequence appearing as ABK91412 and the information in Claim 16

XX Sequence 10690 BP; 2334 A; 3044 C; 2908 G; 2404 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTG 60
Db |||||

QY 61 TCTTACGCGAGAAAGCGTCTAGCCATGGGCTTAGTATAGTGTGCTGCGACCTCCAGGAC 120
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Db |||||

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Db |||||

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Db 7981 AGATCAAGTACT 7992

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RESULT 8

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ABK91243
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AC ABK91243;
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15-NOV-2002 (first entry)
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Hepatitis C virus vector construct pHVNeo.17.m1.
XX
HCV; ss; pHVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX
Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.

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FT /*tag= g
FT /note= "Plasmid derived sequences"
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W0200259321-A2.

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PR 23-JAN-2001; 2001US-0263479P.
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PA (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
XX
PI De Francesco R, Migliaccio G, Paonessa G;
XX MPI; 2002-599793/64.
XX
PT New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.
XX
PS Example 1; Page; 69pp; English.
XX
CC The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC ; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replicons and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and HCV and host cell interactions, producing HCV RNA and
CC proteins, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is an HCV based vector
CC pHVNeo.17 mutant of the invention. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the HCV
CC vector sequence appearing as ABK91412 and the information in example 1
XX
SQ Sequence 10690 BP; 2333 A; 3046 C; 2908 G; 2403 T; 0 U; 0 Other;

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Query Match 100.0%; Score 7990.4; DB 6; Length 10690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAAGTACTG 60
Db 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAAGTACTG 60

QY 61 TCTTCAGCGAAGAGCGTCTAGCCATGGCGTTAGTAGTAGTGTGCGACGCTCCAGGAC 120
Db 61 TCTTCAGCGAAGAGCGTCTAGCCATGGCGTTAGTAGTAGTGTGCGACGCTCCAGGAC 120

QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTGAGTACACCGGAATGCGAG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTGAGTACACCGGAATGCGAG 180

QY 181 GAGCAGCGGGTCTTCTTGGATCAACCCGCTCAATGCGTGGAGATTGGCGGTGCCCC 240
Db 181 GAGCAGCGGGTCTTCTTGGATCAACCCGCTCAATGCGTGGAGATTGGCGGTGCCCC 240

QY 241 GCGAGACTCTAGCGAGTAGTGTGGGTGCGAAGAGCGCTTGTGTACTGTGCTGATAG 300
Db 241 GCGAGACTCTAGCGAGTAGTGTGGGTGCGAAGAGCGCTTGTGTACTGTGCTGATAG 300

QY 301 GTGCTTGGAGTSCCCCGGAGGTCTCGTAGACCGGTGACACCATGACGACGAATCCTAAC 360
Db 301 GTGCTTGGAGTSCCCCGGAGGTCTCGTAGACCGGTGACACCATGACGACGAATCCTAAC 360

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QY	361	CTCAAGAAAAACCAAGGGCGCGCCATGATGACAAAGATGGATTGACAGGTTCTC	420	Db	1441	GTTCCTCTGGAAGTCTTTGAAACAAACAGCTCTGTAGCGACCTTTGCGAGCGG	1500
Db	361	CTCAAGAAAAACCAAGGGCGCGCCATGATGAAACAAAGATGGATTGACAGGTTCTC	420	QY	1501	AACCCCCCACCCTGGCGACAGGTGCGCTCTGCGGCCAAAAAGCCAGCTGTATAGATACACT	1560
QY	421	CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACACAGACAATCGGCTGT	480	Db	1501	AACCCCCCACCCTGGCGACAGGTGCGCTCTGCGGCCAAAAAGCCAGCTGTATAGATACACT	1560
Db	421	CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACACAGACAATCGGCTGT	480	QY	1561	GCAAAAGGGCGCAACACCCAGTCGCCAGTGTGAGTTCGATAGTGTGGAAGAGTCAAA	1620
QY	481	CTGATGCGCGCTGTTCGCGCTGTGAGCGACAGGGCGCCCGTCTTTTGTTCAGACCG	540	Db	1561	GCAAAAGGGCGCAACACCCAGTCGCCAGTGTGAGTTCGATAGTGTGGAAGAGTCAAA	1620
Db	481	CTGATGCGCGCTGTTCGCGCTGTGAGCGACAGGGCGCCCGTCTTTTGTTCAGACCG	540	QY	1621	TGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAAGGATGCCAGAGTACCCCATTTGT	1680
QY	541	ACCTGTCCGGTGCCCTGAATGAATGACGACGAGGACGCGGCTATCGTGGCTGGCA	600	Db	1621	TGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAAGGATGCCAGAGTACCCCATTTGT	1680
Db	541	ACCTGTCCGGTGCCCTGAATGAATGACGACGAGGACGCGGCTATCGTGGCTGGCA	600	QY	1681	ATGGGATCTGATCTGGGGCTCGGTGCACATCTTTACATGTGTGTAGTCGAGGTTAAAA	1740
QY	601	CGACGGCGCTTCTTGGCAGCTGTCTCGACGTGTCTCACTGAAGCGGGAAGGACTGGC	660	Db	1681	ATGGGATCTGATCTGGGGCTCGGTGCACATCTTTACATGTGTGTAGTCGAGGTTAAAA	1740
Db	601	CGACGGCGCTTCTTGGCAGCTGTCTCGACGTGTCTCACTGAAGCGGGAAGGACTGGC	660	QY	1741	AACGTCTAGGCCCCCGAAACACAGGGGAGTGGTTCCTTTGAAAAACACGATAATACC	1800
QY	661	TGCTATTGGGCGAAGTCCCGGGCAGGATCTCCTGTCACTCACTTGTCTTCCGCGAGA	720	Db	1741	AACGTCTAGGCCCCCGAAACACAGGGGAGTGGTTCCTTTGAAAAACACGATAATACC	1800
Db	661	TGCTATTGGGCGAAGTCCCGGGCAGGATCTCCTGTCACTCACTTGTCTTCCGCGAGA	720	QY	1801	ATGGCGCTATTACGGCTACTCCCAACAGACCGCGAGGCTACTTTGGCTGCATCATCACT	1860
QY	721	AGTATCCATCATGGCTGATGCAATCGCGGCTGCACTGCTGATCCGGCTACCTGCC	780	Db	1801	ATGGCGCTATTACGGCTACTCCCAACAGACCGCGAGGCTACTTTGGCTGCATCATCACT	1860
Db	721	AGTATCCATCATGGCTGATGCAATCGCGGCTGCACTGCTGATCCGGCTACCTGCC	780	QY	1861	AGCTCTCACAGCGCGGACAGGAACACAGGTGCGAGGGGAGSTCCAGTGGTCTCCACGCA	1920
QY	781	CATTTCGACACCAAGCGAAACATCGCATCGAGGAGCACGTACTCGGATGGAAGCCGGTC	840	Db	1861	AGCTCTCACAGCGCGGACAGGAACACAGGTGCGAGGGGAGSTCCAGTGGTCTCCACGCA	1920
Db	781	CATTTCGACACCAAGCGAAACATCGCATCGAGGAGCACGTACTCGGATGGAAGCCGGTC	840	QY	1921	ACAAATCTTCTTGGCGACTGGCTCAATGGCGTGTGGTGTCTATCATGTGGC	1980
QY	841	TTGTTCGATCAGGATGATTCGACAGAGATCAGGGGCTCGCGCAGCGCACTGTCG	900	Db	1921	ACAAATCTTCTTGGCGACTGGCTCAATGGCGTGTGGTGTCTATCATGTGGC	1980
Db	841	TTGTTCGATCAGGATGATTCGACAGAGATCAGGGGCTCGCGCAGCGCACTGTCG	900	QY	1981	GGCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCCAAATGTACAAATGTGGAC	2040
QY	901	CCAGGCTCAAGCGCGCATGCGCGAGGATCTCGTTCGACCATGGCGATGCGT	960	Db	1981	GGCTCAAGACCTTTCGCGCCCAAGGGCCCAATCACCCAAATGTACAAATGTGGAC	2040
Db	901	CCAGGCTCAAGCGCGCATGCGCGAGGATCTCGTTCGACCATGGCGATGCGT	960	QY	2041	CAGGACCTCGTTCGGCTGGCAAGCGCCCGCGGGCGGTTCCTTTGACACCATGACCTGC	2100
QY	961	GCTTTCGCAATCATGCTGGAATGCGCGCTTTCTGGAATCATGACCTGTCGCGGC	1020	Db	2041	CAGGACCTCGTTCGGCTGGCAAGCGCCCGCGGGCGGTTCCTTTGACACCATGACCTGC	2100
Db	961	GCTTTCGCAATCATGCTGGAATGCGCGCTTTCTGGAATCATGACCTGTCGCGGC	1020	QY	2101	GCGAGCTCGGACCTTTACTTGGTCAAGGCGCATCCGATGTCATTCGGTGGCGGCGG	2160
QY	1021	TGGGTGTCGCGACCGCTATCAGGACATAGCGTTGGCTACCGGTATTCGTAAGAGC	1080	Db	2101	GCGAGCTCGGACCTTTACTTGGTCAAGGCGCATCCGATGTCATTCGGTGGCGGCGG	2160
Db	1021	TGGGTGTCGCGACCGCTATCAGGACATAGCGTTGGCTACCGGTATTCGTAAGAGC	1080	QY	2161	GGCGACAGCAGGGGAGCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAAGGGCTCTCG	2220
QY	1081	TTGGGGCGMATGGGCTGACCGCTTTCGCTGCTTTACGGTATCGCGCTCCCGATTGCG	1140	Db	2161	GGCGACAGCAGGGGAGCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAAGGGCTCTCG	2220
Db	1081	TTGGGGCGMATGGGCTGACCGCTTTCGCTGCTTTACGGTATCGCGCTCCCGATTGCG	1140	QY	2221	GGCGGTCACCTGCTCTGCCCTTCGGGGCAACGCTGTGGGCACTTTTCGGGCTGCCGTGTC	2280
QY	1141	AGCGCATCGCTTCTATCGCTTTCGAGGATCTTCTGAGTTTAAACAGACCAACG	1200	Db	2221	GGCGGTCACCTGCTCTGCCCTTCGGGGCAACGCTGTGGGCACTTTTCGGGCTGCCGTGTC	2280
Db	1141	AGCGCATCGCTTCTATCGCTTTCGAGGATCTTCTGAGTTTAAACAGACCAACG	1200	QY	2281	ACCCAGGGGTTGCAAGCGGTGACCTTTGACCCGTCAGTCTATGAAACCACTATG	2340
QY	1201	GTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTGTCG	1260	Db	2281	ACCCAGGGGTTGCAAGCGGTGACCTTTGACCCGTCAGTCTATGAAACCACTATG	2340
Db	1201	GTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACTGTCG	1260	QY	2341	CGGTCCCGGCTTTCACGGACAACCTCTCCCGCTCCGGCGGTACCGCAGACATTCAGGTTG	2400
QY	1261	CGAAGCGCTTGAATAAGCGGCTGCTGCTATGTTATTTTCCACCATATG	1320	Db	2341	CGGTCCCGGCTTTCACGGACAACCTCTCCCGCTCCGGCGGTACCGCAGACATTCAGGTTG	2400
Db	1261	CGAAGCGCTTGAATAAGCGGCTGCTGCTATGTTATTTTCCACCATATG	1320	QY	2401	GCCCATCTACACGCCCTTACTGGTAGCGCAAGACACTAAGGTGCGGCTCGGTATGCA	2460
QY	1321	CGGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTTCTTGAGGAGCTTCT	1380	Db	2401	GCCCATCTACACGCCCTTACTGGTAGCGCAAGACACTAAGGTGCGGCTCGGTATGCA	2460
Db	1321	CGGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTTCTTGAGGAGCTTCT	1380	QY	2461	GCCCAAGGTTATAGGTGCTTGTCTGAAACCGCTCGCGCCGACCCCTAGGTTTCGGG	2520
QY	1381	AGGGGTCTTTCCTCTCGGCAAGGATGCAAGGCTGTGTAATGTCTGTAAGGAGCA	1440	Db	2461	GCCCAAGGTTATAGGTGCTTGTCTGAAACCGCTCGCGCCGACCCCTAGGTTTCGGG	2520
Db	1381	AGGGGTCTTTCCTCTCGGCAAGGATGCAAGGCTGTGTAATGTCTGTAAGGAGCA	1440	QY	2521	GCCTATATGCTTAAGGCAATGGTATCGACCTTAAATCAAGAACCGGGGTGAGGACCATC	2580
QY	1441	GTTCCTCTGGAAGCTTCTTGAAGACAAACACGCTCTGTAGCGACCTTTGCGAGCGG	1500				

Db	2521	GGGTATATGCTTAAGGCACATGTTATCGACCTTAACATCAGAAACCGGGTAAGACCATC	2580
QY	2581	ACCAAGGGTGCCCCCATCACGTACTCCACTATGAGCAAGTTCTTCTCCGACGGTGGTGC	2640
Db	2581	ACCAAGGGTGCCCCCATCACGTACTCCACTATGAGCAAGTTCTTCTCCGACGGTGGTGC	2640
QY	2641	TCTGGGGGCGCTATGACATCATATATGATGTGAGTGCACCTCAACTGACTCGACCACT	2700
Db	2641	TCTGGGGGCGCTATGACATCATATATGATGTGAGTGCACCTCAACTGACTCGACCACT	2700
QY	2701	ATCTTGGGCATCGGCACACAGTCTTGACCAAGCGGAGACGGCTGGAGCGAGCTCGTGG	2760
Db	2701	ATCTTGGGCATCGGCACACAGTCTTGACCAAGCGGAGACGGCTGGAGCGAGCTCGTGG	2760
QY	2761	CTCGCCACCGGTACGCTCCGGATCGGTACCGTGCACATCCCAACATCGAGAGGTTG	2820
Db	2761	CTCGCCACCGGTACGCTCCGGATCGGTACCGTGCACATCCCAACATCGAGAGGTTG	2820
QY	2821	GCTCTGTCCAGCATGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880
Db	2821	GCTCTGTCCAGCATGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC	2880
QY	2881	AAGGGGGGAGGCACCTCATTTCTGCCCATTCCAAAGAAATGTGATCGTCGCGG	2940
Db	2881	AAGGGGGGAGGCACCTCATTTCTGCCCATTCCAAAGAAATGTGATCGTCGCGG	2940
QY	2941	AAGTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGTATTCGGTC	3000
Db	2941	AAGTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGTATTCGGTC	3000
QY	3001	ATACCAACTAGCGGAGACGTATTGTGCTAGCAACGGACGCTCTAATGACGGGCTTTACC	3060
Db	3001	ATACCAACTAGCGGAGACGTATTGTGCTAGCAACGGACGCTCTAATGACGGGCTTTACC	3060
QY	3061	GGCGATTTCGACTCAGTGATCGACTCAATACATGTGTACCCAGACAGTCTCAGC	3120
Db	3061	GGCGATTTCGACTCAGTGATCGACTCAATACATGTGTACCCAGACAGTCTCAGC	3120
QY	3121	CTGGACCGGACCTTCACATTGAGACGACGACCGTGCACAAAGACGGGTGTACGCTCG	3180
Db	3121	CTGGACCGGACCTTCACATTGAGACGACGACCGTGCACAAAGACGGGTGTACGCTCG	3180
QY	3181	CAGCGCGAGGACGAGTGTGTAGGGCAGATGGGCAATTACAGTTTGTGACTCCAGGA	3240
Db	3181	CAGCGCGAGGACGAGTGTGTAGGGCAGATGGGCAATTACAGTTTGTGACTCCAGGA	3240
QY	3241	GAACGGCCCTCGGGCATGTTTCGATTCTCGTTCTGTGCGAGTGTATGACGGGGGTGT	3300
Db	3241	GAACGGCCCTCGGGCATGTTTCGATTCTCGTTCTGTGCGAGTGTATGACGGGGGTGT	3300
QY	3301	GCTTGGTACGAGTACGCGCGCCGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA	3360
Db	3301	GCTTGGTACGAGTACGCGCGCCGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA	3360
QY	3361	CCAGGTTTGGCGTCTGCCAGACCATCTGGAGTTCTGGGAGAGCGTCTTACAGGCTC	3420
Db	3361	CCAGGTTTGGCGTCTGCCAGACCATCTGGAGTTCTGGGAGAGCGTCTTACAGGCTC	3420
QY	3421	ACCCACATAGACGCCATTTCTTGTCCACAGCTTAAGCAGCGAGACAACTTCCCTTAC	3480
Db	3421	ACCCACATAGACGCCATTTCTTGTCCACAGCTTAAGCAGCGAGACAACTTCCCTTAC	3480
QY	3481	CTGTTAGCATACGAGCTACGGTGTGCGCCAGGCTCAGGCTCCACTCCATCGTGGGAC	3540
Db	3481	CTGTTAGCATACGAGCTACGGTGTGCGCCAGGCTCAGGCTCCACTCCATCGTGGGAC	3540
QY	3541	CAATGTGGAAGTGTCTATACGGCTTAAGCCTACGCTGCAAGGGCCAAAGCCCTGCTG	3600
Db	3541	CAATGTGGAAGTGTCTATACGGCTTAAGCCTACGCTGCAAGGGCCAAAGCCCTGCTG	3600
QY	3601	TATAGGCTGGGAGCGGTTCAAACGAGGTTACTACCACACACCCATACCAATATCATC	3660
Db	3601	TATAGGCTGGGAGCGGTTCAAACGAGGTTACTACCACACACCCATACCAATATCATC	3660

QY	3661	ATGGCATGCAATCGCGTGAACCTGGAGGTGCTCACGAGCACCTGGGTGCTGGTAGGCGGA	3720
Db	3661	ATGGCATGCAATGTCGGTGAACCTGGAGGTGCTCACGAGCACCTGGGTGCTGGTAGGCGGA	3720
QY	3721	GTCTAGCAGCTCTGGCGCGTATTGCTTGAACAAGGAGCGGTGTCTATTGTGGGCGAGG	3780
Db	3721	GTCTAGCAGCTCTGGCGCGTATTGCTTGAACAAGGAGCGGTGTCTATTGTGGGCGAGG	3780
QY	3781	ATCATCTTGTTCGGAAAGCGCGCCATCATTCGCCGACAGGGAAGTCTTTACCGGAGTTTC	3840
Db	3781	ATCATCTTGTTCGGAAAGCGCGCCATCATTCGCCGACAGGGAAGTCTTTACCGGAGTTTC	3840
QY	3841	GATGAGATGGAAGTGGCCCTCACACCTCCCTTATCGAAACAGGGAATGCAAGTTCGCC	3900
Db	3841	GATGAGATGGAAGTGGCCCTCACACCTCCCTTATCGAAACAGGGAATGCAAGTTCGCC	3900
QY	3901	GAACAAATTCAAACAGAGGCGAATCGGTTGCTGCAAAAGCCACCAAGCAGCGAGGCT	3960
Db	3901	GAACAAATTCAAACAGAGGCGAATCGGTTGCTGCAAAAGCCACCAAGCAGCGAGGCT	3960
QY	3961	GCTGCTCCGCTGTGTGAATCCAAGTGGCGGACCTCGAAGCTTCTGGCGAAGCATATG	4020
Db	3961	GCTGCTCCGCTGTGTGAATCCAAGTGGCGGACCTCGAAGCTTCTGGCGAAGCATATG	4020
QY	4021	TGGAATTTCTACGCGGGATACAATATTTAGAGGCTTGTCCACTCTGCTGGCAACCCC	4080
Db	4021	TGGAATTTCTACGCGGGATACAATATTTAGAGGCTTGTCCACTCTGCTGGCAACCCC	4080
QY	4081	GCATAGCATCACTGATGGCATTTACAGCTCTATCACAGCCGCTCACACCCCAACAT	4140
Db	4081	GCATAGCATCACTGATGGCATTTACAGAGCTCTATCACAGCCGCTCACACCCCAACAT	4140
QY	4141	ACCTCTCTGTTTAACTCTCGGGGGATGGTGGCGGCCCAACTTCTCTCCAGCGCT	4200
Db	4141	ACCTCTCTGTTTAACTCTCGGGGGATGGTGGCGGCCCAACTTCTCTCCAGCGCT	4200
QY	4201	GCTTCTGCTTTCTAGCGCGCGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTTGGG	4260
Db	4201	GCTTCTGCTTTCTAGCGCGCGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTTGGG	4260
QY	4261	AAGGTGCTTGTGATATTTGGCAGGTTATGGAGAGGGGTGGCAGCGGCTCGTGCC	4320
Db	4261	AAGGTGCTTGTGATATTTGGCAGGTTATGGAGAGGGGTGGCAGCGGCTCGTGCC	4320
QY	4321	TTTAAAGTCAATGAGCGGCGAGATGCCCTCCACGAGGACCTGTTAACTACTCCCTGCT	4380
Db	4321	TTTAAAGTCAATGAGCGGCGAGATGCCCTCCACGAGGACCTGTTAACTACTCCCTGCT	4380
QY	4381	ATCCTCTCCCTGGCGCCCTAGTGTGCGGGTGTGTGGCAGCGATCTGCGTGGGCAC	4440
Db	4381	ATCCTCTCCCTGGCGCCCTAGTGTGCGGGTGTGTGGCAGCGATCTGCGTGGGCAC	4440
QY	4441	GTGGGCCAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGGTTTCGCTTCGCGG	4500
Db	4441	GTGGGCCAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGGTTTCGCTTCGCGG	4500
QY	4501	GGTAAACCAAGTCTCCCCCAGCACTATGTGCTGAGAGCGAGCTGCACAGTGTCACT	4560
Db	4501	GGTAAACCAAGTCTCCCCCAGCACTATGTGCTGAGAGCGAGCTGCACAGTGTCACT	4560
QY	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGTCTGAAGAGGCTTTCACCAAGTGGATCAAC	4620
Db	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGTCTGAAGAGGCTTTCACCAAGTGGATCAAC	4620
QY	4621	GAGACTGCTCCACGCCATGCTCCGGCTCTGGGTGAAGATGTTTGGGATTTGGATATGC	4680
Db	4621	GAGACTGCTCCACGCCATGCTCCGGCTCTGGGTGAAGATGTTTGGGATTTGGATATGC	4680
QY	4681	ACGGTGTGACTGATTTTCAAGACCTGGCTCCAGTCCAGTCTCTGCGGGATTCGCGGA	4740
Db	4681	ACGGTGTGACTGATTTTCAAGACCTGGCTCCAGTCCAGTCTCTGCGGGATTCGCGGA	4740

Db	5821	ACGGCCCTCTCTGACCAAGCCCTCCGACACGCGGATCCGAGCTTGAGTCGTAC	5880
Qy	5881	TCCTCATGCCCCCTTTGAGGGGAGCGGGGATCCGATCTCAGCGACGGGTCTTGG	5940
Db	5881	TCCTCATGCCCCCTTTGAGGGGAGCGGGGATCCGATCTCAGCGACGGGTCTTGG	5940
Qy	5941	TCTACCGTAAGCGAGGAGCTAGTCAGGACGTCGTCTGCTCGATGTCCTACACATGG	6000
Db	5941	TCTACCGTAAGCGAGGAGCTAGTCAGGACGTCGTCTGCTCGATGTCCTACACATGG	6000
Qy	6001	ACAGCGCCCTGATCAACGCAATGCGGTGGGAGGAAACCAAGTCGCCATCAATGCACTG	6060
Db	6001	ACAGCGCCCTGATCAACGCAATGCGGTGGGAGGAAACCAAGTCGCCATCAATGCACTG	6060
Qy	6061	AGCACTCTTTGCTCGTCACCAACAATTTGGTCTATGCTACAACATCTCGCAGCGAAGC	6120
Db	6061	AGCACTCTTTGCTCGTCACCAACAATTTGGTCTATGCTACAACATCTCGCAGCGAAGC	6120
Qy	6121	CTGCGGCAAGAAAGGTCACTTTGACAGCTGACAGTCTGAGACACACTACCGGGAC	6180
Db	6121	CTGCGGCAAGAAAGGTCACTTTGACAGCTGACAGTCTGAGACACACTACCGGGAC	6180
Qy	6181	GTGCTCAAGAGATGAAGGGAAGGCGTCCACAGTTTAAGGCTAAACTTCTATCGCTGGAG	6240
Db	6181	GTGCTCAAGAGATGAAGGGAAGGCGTCCACAGTTTAAGGCTAAACTTCTATCGCTGGAG	6240
Qy	6241	GAAGCCTGTAAGCTGACGCCCCACACATTTGCGCCAGATCTAAATTTGGCTATGGGGCAAG	6300
Db	6241	GAAGCCTGTAAGCTGACGCCCCACACATTTGCGCCAGATCTAAATTTGGCTATGGGGCAAG	6300
Qy	6301	GAGCTCCGGAACCTATCCAGCAAGCGCTTAAACACATCGCTCCGCTGAGAGCACTTG	6360
Db	6301	GAGCTCCGGAACCTATCCAGCAAGCGCTTAAACACATCGCTCCGCTGAGAGCACTTG	6360
Qy	6361	CTGGAAGACACTGAGACACAAATTGACACACCACTCATGSCAAATAATGAGTTTCTGC	6420
Db	6361	CTGGAAGACACTGAGACACAAATTGACACACCACTCATGSCAAATAATGAGTTTCTGC	6420
Qy	6421	GTCCAAACAGAGAAGGGGGCGCAAGCAGCTCGCTTATCGTATTCAGATTTGGGG	6480
Db	6421	GTCCAAACAGAGAAGGGGGCGCAAGCAGCTCGCTTATCGTATTCAGATTTGGGG	6480
Qy	6481	GTTGCTGTGCGAGAAATGCGCTTTACGATGTGCTCTCACCTCCCTCAGGCGGTG	6540
Db	6481	GTTGCTGTGCGAGAAATGCGCTTTACGATGTGCTCTCACCTCCCTCAGGCGGTG	6540
Qy	6541	ATGGCTCTTTCATACGGATTCCAATCTCTCTGACACGGGTGCGAGTTCTGTGTAAT	6600
Db	6541	ATGGCTCTTTCATACGGATTCCAATCTCTCTGACACGGGTGCGAGTTCTGTGTAAT	6600
Qy	6601	GCTCGGAAGCGAAGAAATGCGCTATGGCTTCGATATGACACCGCTGTTTTCACCTCA	6660
Db	6601	GCTCGGAAGCGAAGAAATGCGCTATGGCTTCGATATGACACCGCTGTTTTCACCTCA	6660
Qy	6661	ACGGTCACTGAGAATGACATCGCTGTGAGGAGTCAATCTCAATGTTGTGACTGGCC	6720
Db	6661	ACGGTCACTGAGAATGACATCGCTGTGAGGAGTCAATCTCAATGTTGTGACTGGCC	6720
Qy	6721	CCCGAAGCCAGACAGGCCATAAGTTCGCTCAAGACGCGCTTACATCGGGGCCCTTGG	6780
Db	6721	CCCGAAGCCAGACAGGCCATAAGTTCGCTCAAGACGCGCTTACATCGGGGCCCTTGG	6780
Qy	6781	ACTAATTTAAAGGCGAGACTGCGCTATCGCGGTGCGGCGAGCGGTGTACTGACG	6840
Db	6781	ACTAATTTAAAGGCGAGACTGCGCTATCGCGGTGCGGCGAGCGGTGTACTGACG	6840
Qy	6841	ACCAGCTGCGGTAATACCTTCATATGTAAGGCGCGCTCGGGCTGTCAAGCTGGC	6900
Db	6841	ACCAGCTGCGGTAATACCTTCATATGTAAGGCGCGCTCGGGCTGTCAAGCTGGC	6900
Qy	6901	AAGCTCCAGACTGACGATGCTCGTATCGGAGACGACTTGTGCTTATCTGTGAAGC	6960

Db 6901 AAGCTCCAGACTGCAGGATGCTCGTATGCGGAGACGACCTTCTGTTAFTCTGTGAAGC 6960
QY 6961 GCGGGACCCAGAGGACGAGGAGCGAGCTTACGGGCTTTACGGAGGCTATGACTAGATAC 7020
Db 6961 GCGGGACCCAGAGGACGAGGAGCGAGCTTACGGGCTTTACGGAGGCTATGACTAGATAC 7020
QY 7021 TCTGCCCTCCCTGGGACCGCCCAACAGATACGACTTGGAGTTGATAACATCATGC 7080
Db 7021 TCTGCCCTCCCTGGGACCGCCCAACAGATACGACTTGGAGTTGATAACATCATGC 7080
QY 7081 TCTTCCAATGTGTCACTCGCGACGATCATCTGGCAAAAGGCTGACTATCTCACCCCT 7140
Db 7081 TCTTCCAATGTGTCACTCGCGACGATCATCTGGCAAAAGGCTGACTATCTCACCCCT 7140
QY 7141 GACCCACACCCCTTGGGCGGCTGCGTGGAGACAGCTAGACACACTCCAGTCAAT 7200
Db 7141 GACCCACACCCCTTGGGCGGCTGCGTGGAGACAGCTAGACACACTCCAGTCAAT 7200
QY 7201 TCTGGCTAGGCAACATCATCTAGCTCAGGAACTTGAAGAGCCCTAGATTGTGAG 7260
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Db 7321 ATCTACGGGCTGTATCTCAATGAGCACTTACCTACCTCAGATCATCTCAAGCATC 7380
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Db 7381 CATGGCTTAGGCACTTCTCACTCATAGTACTCTCCAGTGAATCAATAGGCTGCT 7440
QY 7441 TCATGCTCAGGAACTTGGGCTACCGGCTTGGAGTCTGGAGACATCGGGCAGAGT 7500
Db 7441 TCATGCTCAGGAACTTGGGCTACCGGCTTGGAGTCTGGAGACATCGGGCAGAGT 7500
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QY 7561 AACTGGGAGTAAGGACCAAGCTCAACTCACTCAATCCGCTGCTGCCAGTGGAT 7620
Db 7561 AACTGGGAGTAAGGACCAAGCTCAACTCACTCAATCCGCTGCTGCCAGTGGAT 7620
QY 7621 TTATPCAGCTGGTTCGTGTGCTTACAGGGGGAGACATATACAGCTGTCTCGT 7680
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QY 7681 GCGGACCCGCTGGTTCATGTGCTGCTACTCTTCTGTAGGGTAGGCACTAT 7740
Db 7681 GCGGACCCGCTGGTTCATGTGCTGCTACTCTTCTGTAGGGTAGGCACTAT 7740
QY 7741 CTACTCCCAACCGAGGAGCGGAGCTAAACACTCAGGCCAATAGGCCATCTGTTT 7800
Db 7741 CTACTCCCAACCGAGGAGCGGAGCTAAACACTCAGGCCAATAGGCCATCTGTTT 7800
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
QY 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
QY 7921 TAGCTGTGAAGTCCGTGAGCGCTTGTGCTGAGAGTGTGATCTGCGCTCTCTGC 7980
Db 7921 TAGCTGTGAAGTCCGTGAGCGCTTGTGCTGAGAGTGTGATCTGCGCTCTCTGC 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 9
ABK91434
ID ABK91434 standard; DNA; 10690 BP.
XX
AC ABK91434;
XX
DT 15-NOV-2002 (first entry)
XX
DE Hepatitis C virus vector construct pHCVNeo.17m0.
XX
KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX
OS Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..341
FT /tag= a
FT CDS 342..1181
FT /tag= b
FT /product= "Core-neo fusion protein"
FT misc_signal 1190..1800
FT /tag= c
FT /label= IRES
FT /note= "Internal ribosome entry site from EMCV"
FT CDS 1801..7758
FT /tag= d
FT /product= "Polyprotein"
FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
FT mutation replace(5337,C)
FT /tag= e
FT 3'UTR 7759..7991
FT /tag= f
FT misc_feature 7992..10690
FT /tag= g
FT /note= "Plasmid derived sequences"
W0200259321-A2.
XX
PD 01-AUG-2002.
XX
XX 16-JAN-2002; 2002MO-EP000526.
XX
XX 23-JAN-2001; 2001US-0263479P.
XX
XX (RICE-) IST RICERHC BIOL MOLECOLARE ANGELETTI.
XX
XX De Francesco R, Migliaccio G, Paonessa G;
XX WPI; 2002-599793/64.
XX
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX
XX Claim 16; Page; 69pp; English.
XX
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids

; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV replicon enhanced cells are useful in studying HCV replication and expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV based vector pHCVneo.17 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV vector sequence appearing as ABK91412 and the information in Claim 16

XX Sequence 10690 BP; 2335 A; 3044 C; 2908 G; 2403 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCGATGGGGCGACACCTCCACATAGATCACTCCCTGTGAGGAATACTG 60

DB 1 GCCAGCCCCGATGGGGCGACACCTCCACATAGATCACTCCCTGTGAGGAATACTG 60

QY 61 TCTTACGCAAGAAAGCGTCTAGCGATGCGGCTTGTAGTGTGCTGACGCTCCAGGAC 120

DB 61 TCTTACGCAAGAAAGCGTCTAGCGATGCGGCTTGTAGTGTGCTGACGCTCCAGGAC 120

QY 121 CCCCCCTCCGGAGAGCCATAGTGTCTCGGAACCGGTGAGTACACCGGAATGCGAG 180

DB 121 CCCCCCTCCGGAGAGCCATAGTGTCTCGGAACCGGTGAGTACACCGGAATGCGAG 180

QY 181 GACACCGGCTCTTCTTGATCAACCCGCTCAATCCCTGAGATTTGGCGTGCCTCC 240

DB 181 GACACCGGCTCTTCTTGATCAACCCGCTCAATCCCTGAGATTTGGCGTGCCTCC 240

QY 241 GCGAGATGTGAGCGAGTAGTGTGGTCCGGAAGCCCTGTGACTCCCTGATAGG 300

DB 241 GCGAGATGTGAGCGAGTAGTGTGGTCCGGAAGCCCTGTGACTCCCTGATAGG 300

QY 301 CTCAAGAAAAACCAAGGGCGCCATGATGAAACAGATGGATGCAACGAGTCTC 420

DB 301 CTCAAGAAAAACCAAGGGCGCCATGATGAAACAGATGGATGCAACGAGTCTC 420

QY 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGATGGGCAACAGCAATCGGCTGCT 480

DB 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGATGGGCAACAGCAATCGGCTGCT 480

QY 481 CTGATGCGCGCTGTTCCGGCTGTGAGCGAGGGCGCCGGTCTCTTTTGTCAAGACG 540

DB 481 CTGATGCGCGCTGTTCCGGCTGTGAGCGAGGGCGCCGGTCTCTTTTGTCAAGACG 540

QY 541 ACCTGTCCGGTCCCTGAAATGAATCTGAGGAAGAGCGCGGCTATCGTGGCTGGCA 600

DB 541 ACCTGTCCGGTCCCTGAAATGAATCTGAGGAAGAGCGCGGCTATCGTGGCTGGCA 600

QY 601 CGACGGCGCTTCTTGGCGAGCTGTGCTGAGCTGATGCTGAGCGGAAGGACTGGC 660

DB 601 CGACGGCGCTTCTTGGCGAGCTGTGCTGAGCTGATGCTGAGCGGAAGGACTGGC 660

QY 661 TGTATATGGCGAAGTGGCGGCGAGGATCTCTGTCATCTCACTTGTCTCTGCGCAGA 720

DB 661 TGTATATGGCGAAGTGGCGGCGAGGATCTCTGTCATCTCACTTGTCTCTGCGCAGA 720

QY 721 AAGTATCCATCATGGCTGATGAAATGGCGGCTGATAGCTTGGCTACCTGCC 780

DB 721 AAGTATCCATCATGGCTGATGAAATGGCGGCTGATAGCTTGGCTACCTGCC 780

781 CATTGACCAACAAGCGAAACATCGCATCGAGCGACAGTACTCGGATGAAGCGGTC 840

DB CATTGACCAACAAGCGAAACATCGCATCGAGCGACAGTACTCGGATGAAGCGGTC 840

QY 841 TTGTGATCAGATGATCTGACGAAGAGCATCAGGGCTCGCGCAGCCGAACTGTTG 900

DB 841 TTGTGATCAGATGATCTGACGAAGAGCATCAGGGCTCGCGCAGCCGAACTGTTG 900

QY 901 CCAGGCTCAAGCGCGCATGCCCGGAGGATCTCGTGTGACCCATGCGGATGCT 960

DB 901 CCAGGCTCAAGCGCGCATGCCCGGAGGATCTCGTGTGACCCATGCGGATGCT 960

QY 961 GTTGGCGAATATCATGTGGAATGCGGCTTTCTGATTCATCGACTGTGGCGGC 1020

DB 961 GTTGGCGAATATCATGTGGAATGCGGCTTTCTGATTCATCGACTGTGGCGGC 1020

QY 1021 TGGGTGTGGCGGACGCTATCAGGACATAGCGTTGGCTACCCGCTGATATTGCTGAAGAG 1080

DB 1021 TGGGTGTGGCGGACGCTATCAGGACATAGCGTTGGCTACCCGCTGATATTGCTGAAGAG 1080

QY 1081 TTGGCGCGAATGGGCTGACCGCTTCTGAGGATTTCTGAGTTTAAACAGACCAACG 1140

DB 1081 TTGGCGCGAATGGGCTGACCGCTTCTGAGGATTTCTGAGTTTAAACAGACCAACG 1140

QY 1141 AGCGATCGCTTCTATCGCTTCTTGAAGGATTTCTGAGTTTAAACAGACCAACG 1200

DB 1141 AGCGATCGCTTCTATCGCTTCTTGAAGGATTTCTGAGTTTAAACAGACCAACG 1200

QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTTCTCCCTCCCGCTCCCGCTTACGTTGCG 1260

DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCTTCTCCCTCCCGCTCCCGCTTACGTTGCG 1260

QY 1261 CGAAGCGCTTGAATTAAGCGGCTGCTGCTTCTATGTTTATTTTCCACCATATG 1320

DB 1261 CGAAGCGCTTGAATTAAGCGGCTGCTGCTTCTATGTTTATTTTCCACCATATG 1320

QY 1321 CGGCTTCTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTTCTTGAAGAGGATG 1380

DB 1321 CGGCTTCTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTTCTTGAAGAGGATG 1380

QY 1381 AGGGGTCTTTCCCTCTCGCAAGAGGATCAAGGCTGTTGATGCTGTAAGAGGATG 1440

DB 1381 AGGGGTCTTTCCCTCTCGCAAGAGGATCAAGGCTGTTGATGCTGTAAGAGGATG 1440

QY 1441 GTTCTCTGGAAGCTTCTGGAAGCAAAACAGCTGTAGCGACCTTTGAGGCGGCG 1500

DB 1441 GTTCTCTGGAAGCTTCTGGAAGCAAAACAGCTGTAGCGACCTTTGAGGCGGCG 1500

QY 1501 AACCCCCCTGCGGAGCTGCTCGCGCCAAAGAGCAAGCTGTATAGATACCT 1560

DB 1501 AACCCCCCTGCGGAGCTGCTCGCGCCAAAGAGCAAGCTGTATAGATACCT 1560

QY 1561 GCMAAGGCGGCAACACCCAGTGCCTCGCGCCAAAGAGCAAGCTGTATAGATACCT 1620

DB 1561 GCMAAGGCGGCAACACCCAGTGCCTCGCGCCAAAGAGCAAGCTGTATAGATACCT 1620

QY 1621 TGGCTCTCTCAAGGCTTCTGGAAGGCTGGAAGGATGCGGAGGATGCGGAGGATG 1680

DB 1621 TGGCTCTCTCAAGGCTTCTGGAAGGCTGGAAGGATGCGGAGGATGCGGAGGATG 1680

QY 1681 ATGGGATCTGATCTGGGCTCGGTGCACTGTTTACATGTTTGTAGTGGAGTTAAA 1740

DB 1681 ATGGGATCTGATCTGGGCTCGGTGCACTGTTTACATGTTTGTAGTGGAGTTAAA 1740

QY 1741 AACGCTTAGGCGGCGGAAACACCGGAGCTGGTCTTCTTGAAGAACACGATATACC 1800

DB 1741 AACGCTTAGGCGGCGGAAACACCGGAGCTGGTCTTCTTGAAGAACACGATATACC 1800

QY 1801 ATGGGCGCTTATAGCGCTTCTCCCAAGAGCGGAGGCTTCTTGGCTGCTATCACT 1860

DB 1801 ATGGGCGCTTATAGCGCTTCTCCCAAGAGCGGAGGCTTCTTGGCTGCTATCACT 1860

QY 1861 AGGCTCACAGCGCGGAGCAAGAACAGGCTGAGGGGGAGGCTCCAGTGGTCTCCACGCA 1920

Db 1861 AGCCTCACAGCCGCGGACAGAAACCAAGTGCAGGGGAGGTCCAAGTGGTCTCCACCGCA 1920
QY 1921 ACACAATCTTTCTGGCGACTCGTCAATGGCGTGTGTGGACTGTCTATCATGTGGCC 1980
Db 1921 ACACAATCTTTCTGGCGACTCGTCAATGGCGTGTGTGGACTGTCTATCATGTGGCC 1980
QY 1981 GGCCTAAAGACCCTTGC CGGCCCCAAGGGCCCCAATCACCCAAATGTACACCAATGTGGAC 2040
Db 1981 GGCCTAAAGACCCTTGC CGGCCCCAAGGGCCCCAATCACCCAAATGTACACCAATGTGGAC 2040
QY 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCGTCTTGTACACCATGCACCTGC 2100
Db 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCGTCTTGTACACCATGCACCTGC 2100
QY 2101 GGCAGCTCGGACTTTACTTGGTACAGAGGCATGCCGATGTCAATCCGGTGGCGCGCGG 2160
Db 2101 GGCAGCTCGGACTTTACTTGGTACAGAGGCATGCCGATGTCAATCCGGTGGCGCGCGG 2160
QY 2161 GGCAGCAGCAGGGGAGCCTACTCTCCCGACGGCCGCTCTCTACTTGAAGGCTCTTCG 2220
Db 2161 GGCAGCAGCAGGGGAGCCTACTCTCCCGACGGCCGCTCTCTACTTGAAGGCTCTTCG 2220
QY 2221 GCGCGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCACTTTTCGGCTGCCGTGTGC 2280
Db 2221 GCGCGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCACTTTTCGGCTGCCGTGTGC 2280
QY 2281 ACCGAGGGGTTGCAAGCGGCTGACTTTGTACCCGCTCGAGTCTATGCAAAACCACTATG 2340
Db 2281 ACCGAGGGGTTGCAAGCGGCTGACTTTGTACCCGCTCGAGTCTATGCAAAACCACTATG 2340
QY 2341 CGGTCCCCGGTCTTACAGGCAAACTCGTCCCTCGCGCGGTACCGACACATTCACGGTG 2400
Db 2341 CGGTCCCCGGTCTTACAGGCAAACTCGTCCCTCGCGCGGTACCGACACATTCACGGTG 2400
QY 2401 GCCCATCTACACGCCCTACTGTTAGCGGACAGCATAAGTGCCTGGCTGGGATGCA 2460
Db 2401 GCCCATCTACACGCCCTACTGTTAGCGGACAGCATAAGTGCCTGGCTGGGATGCA 2460
QY 2461 GCCAAGGGTATAAGGTCTTGTCTGCAACCCGTCGTCGCGCCACCCCTAGTCTTCGGG 2520
Db 2461 GCCAAGGGTATAAGGTCTTGTCTGCAACCCGTCGTCGCGCCACCCCTAGTCTTCGGG 2520
QY 2521 GCGTATATGCTAAGGCACATGTTATGCAACCCGTCGTCGCGCCACCCCTAGTCTTCGGG 2580
Db 2521 GCGTATATGCTAAGGCACATGTTATGCAACCCGTCGTCGCGCCACCCCTAGTCTTCGGG 2580
QY 2581 ACCACGGGTGCCCCATCAGCTACTCCACCTATGGCAAGTCTTTCGCGACGGTGTGC 2640
Db 2581 ACCACGGGTGCCCCATCAGCTACTCCACCTATGGCAAGTCTTTCGCGACGGTGTGC 2640
QY 2641 TCTGGGGCGCCTATGACATCAATAATATGTAGTGGCCACTCAACTGACTCGACCACT 2700
Db 2641 TCTGGGGCGCCTATGACATCAATAATATGTAGTGGCCACTCAACTGACTCGACCACT 2700
QY 2701 ATCTGGGATCGGCACAGTCTCGGACAAAGCGGACGCTGGAGCGCACTCGTGTG 2760
Db 2701 ATCTGGGATCGGCACAGTCTCGGACAAAGCGGACGCTGGAGCGCACTCGTGTG 2760
QY 2761 CTGCCACCGCTACGCTCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGGAGTG 2820
Db 2761 CTGCCACCGCTACGCTCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGGAGTG 2820
QY 2821 GCTCTGTCCAGCATGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACCATC 2880
Db 2821 GCTCTGTCCAGCATGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACCATC 2880
QY 2881 AAGGGGGGAGGACCTCATTTTCTGCAATCCAAAGAAATGTGATGAGCTCGCGCG 2940
Db 2881 AAGGGGGGAGGACCTCATTTTCTGCAATCCAAAGAAATGTGATGAGCTCGCGCG 2940
QY 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATATACGGGGCCTTGATGTATCCGTC 3000
Db 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATATACGGGGCCTTGATGTATCCGTC 3000

Db 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATATACGGGGCCTTGATGTATCCGTC 3000
QY 3001 ATACCAACTAGCGGAGACGTCATTTGTGTAGCAACGGAACGCTCTAATGACGGGCTTTACC 3060
Db 3001 ATACCAACTAGCGGAGACGTCATTTGTGTAGCAACGGAACGCTCTAATGACGGGCTTTACC 3060
QY 3061 GCGGATTTTCGACTCAGTGTATGACTGCAATATCATGTGTCAACGAGACGTCGACTTCAG 3120
Db 3061 GCGGATTTTCGACTCAGTGTATGACTGCAATATCATGTGTCAACGAGACGTCGACTTCAG 3120
QY 3121 CTGGACCCGACCTTACCAATTCAGAGACGACGCTGCCACAGACGCGGTGTACGCTCG 3180
Db 3121 CTGGACCCGACCTTACCAATTCAGAGACGACGCTGCCACAGACGCGGTGTACGCTCG 3180
QY 3181 CAGCGCGAGGACGAGTCTGGTAGGGGACGATGGGCAITTTACAGGTTTGTGATCTCCAGGA 3240
Db 3181 CAGCGCGAGGACGAGTCTGGTAGGGGACGATGGGCAITTTACAGGTTTGTGACTCCAGGA 3240
QY 3241 GAACGGCCCTCGGGCATGTTTCAATTCCTCGGTTCTGTGCGAGTGTATGACGGGCTGT 3300
Db 3241 GAACGGCCCTCGGGCATGTTTCAATTCCTCGGTTCTGTGCGAGTGTATGACGGGCTGT 3300
QY 3301 GCTTGTGACGAGCTCACGCCCGCGGACCTCAGTGTAGGTTCTGGGAGGCTCTTAAACACA 3360
Db 3301 GCTTGTGACGAGCTCACGCCCGCGGACCTCAGTGTAGGTTCTGGGAGGCTCTTAAACACA 3360
QY 3361 CAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGGCTCTTAAACACA 3420
Db 3361 CAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGGCTCTTAAACACA 3420
QY 3421 ACCCACAATAGAGCCCATTTCTGTCCAGACTTAAGCAGGACGAGAGCAACTTCCCTTAC 3480
Db 3421 ACCCACAATAGAGCCCATTTCTGTCCAGACTTAAGCAGGAGGAGAGCAACTTCCCTTAC 3480
QY 3481 CTGTGTAGCATACAGGCTACCGTGTGGCCAGGCTCAGGCTCCACCTCCATCTGTGGAC 3540
Db 3481 CTGTGTAGCATACAGGCTACCGTGTGGCCAGGCTCAGGCTCCACCTCCATCTGTGGAC 3540
QY 3541 CAATGTGGAAAGTGTCTCATACGCTAAAGCTTAGCTGACGGGCCAACGCCCTGTGTG 3600
Db 3541 CAATGTGGAAAGTGTCTCATACGCTAAAGCTTAGCTGACGGGCCAACGCCCTGTGTG 3600
QY 3601 TATAGGCTGGGAGCCGTTCAAAACAGGTTACTACACACACCCCAATAACATACATC 3660
Db 3601 TATAGGCTGGGAGCCGTTCAAAACAGGTTACTACACACACCCCAATAACATACATC 3660
QY 3661 ATGSCATGCAATGTCGGCTGACCTGAGGTGCTACGAGGCTCAGGCTGGGTAGGCGGA 3720
Db 3661 ATGSCATGCAATGTCGGCTGACCTGAGGTGCTACGAGGCTCAGGCTGGGTAGGCGGA 3720
QY 3721 GTCTTAGCAGCTCTGGCGCGTATTTGCTGACAAACAGGACGCTGCTTATTTGGGCGAG 3780
Db 3721 GTCTTAGCAGCTCTGGCGCGTATTTGCTGACAAACAGGACGCTGCTTATTTGGGCGAG 3780
QY 3781 ATCATCTGTCCGAAAGCGGCTCATCTCCGAGGAAAGTCTTTTACCGGAGTTC 3840
Db 3781 ATCATCTGTCCGAAAGCGGCTCATCTCCGAGGAAAGTCTTTTACCGGAGTTC 3840
QY 3841 GATGAGATGGAAGAGTGGGCTCACACCTCCCTTACATGCAACAGGAAATGCAGCTGCC 3900
Db 3841 GATGAGATGGAAGAGTGGGCTCACACCTCCCTTACATGCAACAGGAAATGCAGCTGCC 3900
QY 3901 GAACAAATTCAGAGGCAATTCGGGTTCTGCAACAGGACCAACAGCAAGCGGAGCT 3960
Db 3901 GAACAAATTCAGAGGCAATTCGGGTTCTGCAACAGGACCAACAGCAAGCGGAGCT 3960
QY 3961 GCTGCTCCCGTGTGCAATCCAAAGTGGCGGACCTCGAAGCTTCTGGCGAAGCATATG 4020
Db 3961 GCTGCTCCCGTGTGCAATCCAAAGTGGCGGACCTCGAAGCTTCTGGCGAAGCATATG 4020
QY 4021 TGGAAATTTTCATCAGCGGGATACAAATTTTAGCAGGCTTCTCCACTCTGCTGGCAACCC 4080
Db 4021 TGGAAATTTTCATCAGCGGGATACAAATTTTAGCAGGCTTCTCCACTCTGCTGGCAACCC 4080

QY	5161	ACATTTCTGTGTCGGGCTCAATCAATACATCTGTTGGTCAACAGCTCCCATGCGAGCCCGAA	5220
DB	5161	ACATTTCTGTGTCGGGCTCAATCAATACATCTGTTGGTCAACAGCTCCCATGCGAGCCCGAA	5220
QY	5221	CCGACGCTAGCAGTGCTCATTCTCATGTCTACCGACCCCTCCCATATTACGGCGGAGACG	5280
DB	5221	CCGACGCTAGCAGTGCTCATTCTCATGTCTACCGACCCCTCCCATATTACGGCGGAGACG	5280
QY	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCCCCTCTCTGGCCAGCTCATCAGCTAGCCAG	5340
DB	5281	GCTAAGCGTAGGCTGGCCAGGGGATCTCCCCCTCTCTGGCCAGCTCATCAGCTAGCCAG	5340
QY	5341	CTGCTCTGGCCTTCTCTTGAAGGCAACATGCATACCCGTCTATGACTCCCGGACGCTGAC	5400
DB	5341	CTGCTCTGGCCTTCTCTTGAAGGCAACATGCATACCCGTCTATGACTCCCGGACGCTGAC	5400
QY	5401	CTCATCGAGGCCAACTCTCTGTGGCGCAGGAGATGGCGGGGAAATACACCCCGTGGAG	5460
DB	5401	CTCATCGAGGCCAACTCTCTGTGGCGCAGGAGATGGCGGGGAAATACACCCCGTGGAG	5460
QY	5461	TCAGAAATAAGGTAGTAAATTTTGGACTCTTTTCAGCCGCTCCAAAGCGGAGGAGATGAG	5520
DB	5461	TCAGAAATAAGGTAGTAAATTTTGGACTCTTTTCAGCCGCTCCAAAGCGGAGGAGATGAG	5520
QY	5521	AGGGAAGTATCCGTTTCGGCGGAGATTCCTCGGAGGTTCAGGAAATTCCTTCGAGCGATG	5580
DB	5521	AGGGAAGTATCCGTTTCGGCGGAGATTCCTCGGAGGTTCAGGAAATTCCTTCGAGCGATG	5580
QY	5581	CCCATATGGCGACGCCCGGANTTACAACCTTCCACTGTTAGAGTCTCGAAGGACCCCGAC	5640
DB	5581	CCCATATGGCGACGCCCGGANTTACAACCTTCCACTGTTAGAGTCTCGAAGGACCCCGAC	5640
QY	5641	TAGTCCCTCCAGTGTACACGGGTGTCCATTCGCGCTGCCAAAGGCCCTCCGATACCA	5700
DB	5641	TAGTCCCTCCAGTGTACACGGGTGTCCATTCGCGCTGCCAAAGGCCCTCCGATACCA	5700
QY	5701	CTTCCACGGAGGAAGGACGCTTGTCTCTCGAAGATCTACCGTGTCTTCTGCTTGGCG	5760
DB	5701	CTTCCACGGAGGAAGGACGCTTGTCTCTCGAAGATCTACCGTGTCTTCTGCTTGGCG	5760
QY	5761	GAGCTCGCCAACAAAGACCTTCGGCAGCTCCGAAATCGTCGGCCGTGCAGCGGCACCGCA	5820
DB	5761	GAGCTCGCCAACAAAGACCTTCGGCAGCTCCGAAATCGTCGGCCGTGCAGCGGCACCGCA	5820
QY	5821	ACGGCCTCTCTGACACAGCCCTCCGACAGCGCGACGCGGATCCGAGCTTGAGTCTGAT	5880
DB	5821	ACGGCCTCTCTGACACAGCCCTCCGACAGCGCGACGCGGATCCGAGCTTGAGTCTGAT	5880
QY	5881	TCCTTCCATGCCCCCTTTGAGGGGAGCCGGGGATCCCGATCTCAGCGACGGGCTTGG	5940
DB	5881	TCCTTCCATGCCCCCTTTGAGGGGAGCCGGGGATCCCGATCTCAGCGACGGGCTTGG	5940
QY	5941	TCTACCGTAACGAGGAGGCTAGTGAGACGTCGTCTGCTGCTCATGCTCTTACACATGG	6000
DB	5941	TCTACCGTAACGAGGAGGCTAGTGAGACGTCGTCTGCTGCTCATGCTCTTACACATGG	6000
QY	6001	ACAGCGCCCTGATCAGCCATCGCTCGGAGGAAACCAAGCTGCCATCAATGACCTG	6060
DB	6001	ACAGCGCCCTGATCAGCCATCGCTCGGAGGAAACCAAGCTGCCATCAATGACCTG	6060
QY	6061	AGCAACTCTTTGCTCCGTCACCAACCTTGTGCTATGTCTAACATCTCGACGCGCAAGC	6120
DB	6061	AGCAACTCTTTGCTCCGTCACCAACCTTGTGCTATGTCTAACATCTCGACGCGCAAGC	6120
QY	6121	CTGCGGCAGAGAAGGTCACCTTTGACAGACTGCGAGTCTCGAGGACCTTACCGGAC	6180
DB	6121	CTGCGGCAGAGAAGGTCACCTTTGACAGACTGCGAGTCTCGAGGACCTTACCGGAC	6180
QY	6181	GTGCTCAAGGAGATCAAGCGGAAGCGCTCCACAGTTTAAGGCTTAACTTATCCGTGGAG	6240
DB	6181	GTGCTCAAGGAGATCAAGCGGAAGCGCTCCACAGTTTAAGGCTTAACTTATCCGTGGAG	6240
QY	6241	GAAGCCTGTAAAGCTGACGCCCCCAACATTCGCGCAGATCTTAAATTTGGCTATGGGCCAAG	6300

Db 6241 GAAGCCTGTAAAGCTGACGCCCCACATTCGCGCAGATCTAAATTTGGCTATGCGGCAAAAG 6300
QY 6301 GAGCTCGGAACCTATTCAGCAAGGCGGTAAACCAATCCGCTCCGCTGTCGAAGGACTTG 6360
Db 6301 GAGCTCGGAACCTATTCAGCAAGGCGGTAAACCAATCCGCTCCGCTGTCGAAGGACTTG 6360
QY 6361 CTGGAAGACTGAGACACCAATTTGACACCAATCATGSCAAAATAAGGTTTTCTGC 6420
Db 6361 CTGGAAGACTGAGACACCAATTTGACACCAATCATGSCAAAATAAGGTTTTCTGC 6420
QY 6421 GTCACACAGAGAAAGGCGCGCAAGCCAGCTCGCTTATCGTATCCAGATTTGGGG 6480
Db 6421 GTCACACAGAGAAAGGCGCGCAAGCCAGCTCGCTTATCGTATCCAGATTTGGGG 6480
QY 6481 GTTCGTGTGTGCGAGAAATGSCCTTTTACGATGTGGTCTCCACCCCTCCCTCAGGCGCGTG 6540
Db 6481 GTTCGTGTGTGCGAGAAATGSCCTTTTACGATGTGGTCTCCACCCCTCCCTCAGGCGCGTG 6540
QY 6541 ATGGGCTCTTCATACGGATTCGAATCTCTCTGGACAGCGGTGAGTTCTGTGTAAT 6600
Db 6541 ATGGGCTCTTCATACGGATTCGAATCTCTCTGGACAGCGGTGAGTTCTGTGTAAT 6600
QY 6601 GCCTGGAAGCGAAGAAATGCGCTATGGGCTTCGCATATGACACCGCTGTTTGACTCA 6660
Db 6601 GCCTGGAAGCGAAGAAATGCGCTATGGGCTTCGCATATGACACCGCTGTTTGACTCA 6660
QY 6661 ACGGTCACTGAGAATGACATCCGTGTGTAGGAGTCAATCTACCAATGTTGTACCTTGCC 6720
Db 6661 ACGGTCACTGAGAATGACATCCGTGTGTAGGAGTCAATCTACCAATGTTGTACCTTGCC 6720
QY 6721 CCCGAAGCCAGACAGCCATAGGTGCGTACAGAGCGGCTTTACATCGGGGCGCCCTG 6780
Db 6721 CCCGAAGCCAGACAGCCATAGGTGCGTACAGAGCGGCTTTACATCGGGGCGCCCTG 6780
QY 6781 ACTAATCTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGGCGCGGCGGCTGTA 6840
Db 6781 ACTAATCTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGGCGCGGCGGCTGTA 6840
QY 6841 ACCAGTCCGGTAAATACCTCAGATGTTACTTGAAGCGCGTTCGCGGCTGCGAGCTCG 6900
Db 6841 ACCAGTCCGGTAAATACCTCAGATGTTACTTGAAGCGCGTTCGCGGCTGCGAGCTCG 6900
QY 6901 AAGCTCCAGAGTGCACATGCTGTATGCGGAGACGACCTTGTGTTATCTGTGAAGC 6960
Db 6901 AAGCTCCAGAGTGCACATGCTGTATGCGGAGACGACCTTGTGTTATCTGTGAAGC 6960
QY 6961 GCGGGACCCAAAGGAGCGAGCGGCTATCGGCGCTTACGAGTGGAGTGAATAACATCATGC 7020
Db 6961 GCGGGACCCAAAGGAGCGAGCGGCTATCGGCGCTTACGAGTGGAGTGAATAACATCATGC 7020
QY 7021 TCTGCCCCCTGCGGACCCGCGCAACCAACAGATACGACTTGGAGTGGATGAATAACATCATGC 7080
Db 7021 TCTGCCCCCTGCGGACCCGCGCAACCAACAGATACGACTTGGAGTGGATGAATAACATCATGC 7080
QY 7081 TCTCCATGTCAGTTCGCGGACGATGCTGTGCGGAGACGACCTTGTGTTATCTGTGAAGC 7140
Db 7081 TCTCCATGTCAGTTCGCGGACGATGCTGTGCGGAGACGACCTTGTGTTATCTGTGAAGC 7140
QY 7141 GACCCACCAACCCCTTGTGCGGCGGCTGCGTGGAGACAGCTAGACACCTCCAGTCAAT 7200
Db 7141 GACCCACCAACCCCTTGTGCGGCGGCTGCGTGGAGACAGCTAGACACCTCCAGTCAAT 7200
QY 7201 TCTGGCTAGGCAACATCATGATGTCGCCACCTTGTGGCAAGGATGATCCCTGATG 7260
Db 7201 TCTGGCTAGGCAACATCATGATGTCGCCACCTTGTGGCAAGGATGATCCCTGATG 7260
QY 7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGAAACACTTGAAGGCGCTAGATTTGTGAG 7320
Db 7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGAAACACTTGAAGGCGCTAGATTTGTGAG 7320
QY 7321 ATCTACGGGCGCTGTACTCCATGAGCCACTTGACCTACTCAGATCATTTCAAGCACTC 7380

Db 7321 ATCTACGGGCGCTGTACTCCATTTAGGACCACTTGACCTACTCAGATCATTTCAAGCACTC 7380
QY 7381 CATGGCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
Db 7381 CATGGCCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
QY 7441 TCATGCTCAGGAAACTTGGGGTACCGCTTCCGAGTCTGGAGACATCGGGCCAGAAGT 7500
Db 7441 TCATGCTCAGGAAACTTGGGGTACCGCTTCCGAGTCTGGAGACATCGGGCCAGAAGT 7500
QY 7501 GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
Db 7501 GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
QY 7561 AACTGGGCAATGAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTCGTCCCAGTTGGAT 7620
Db 7561 AACTGGGCAATGAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTCGTCCCAGTTGGAT 7620
QY 7621 TTATCCAGCTGGTTCGTTGCTGGTTACAGCGGGGAGACATATACAGCCTGTCTCGT 7680
Db 7621 TTATCCAGCTGGTTCGTTGCTGGTTACAGCGGGGAGACATATACAGCCTGTCTCGT 7680
QY 7681 GCCGACCCCGCTGCTTCATGTGGTGCCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT 7740
Db 7681 GCCGACCCCGCTGCTTCATGTGGTGCCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT 7740
QY 7741 CTACTCCCAACCGATGAAACCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT 7800
Db 7741 CTACTCCCAACCGATGAAACCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT 7800
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 7920
Db 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 7920
QY 7921 TAGCTGTAAAGGTCGCGTACCGCTTGAAGTGTGACGTGACAGAGTGTGATCTGGCTCTCTGC 7980
Db 7921 TAGCTGTAAAGGTCGCGTACCGCTTGAAGTGTGACGTGACAGAGTGTGATCTGGCTCTCTGC 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 10
ADP86264
ID ADP86264 standard; DNA; 11313 BP.
XX AC ADP86264;
XX DT 23-SEP-2004 (first entry)
XX DE Hepatitis C virus Con-1 replicon I377/NS3-3' plasmid DNA.
XX KW Hepatitis C virus; HCV; anti-HCV agent; HCV infection; therapy; plasmid;
XX OS ds.
XX OS Hepatitis C virus.
XX PN WO2004055216-A2.
XX PD 01-JUL-2004.
XX PF 12-DEC-2003; 2003WO-US039722.
XX PR 13-DEC-2002; 2002US-0433303P.
XX PA (FOXC-) FOX CHASE CANCER CENT.
XX PI Zhu Q, Guo J, Seeger C;

XX	WPI; 2004-498079/46.
DR	GENBANK; AJ242652.
DR	
PT	New cell-line that replicates hepatitis C virus (HCV), where the cell
PT	line is selected from a non-human cell line and a human non-hepatic cell
PT	line, useful for identifying anti-HCV agents for treating HCV infections.
XX	
XX	Example III; SEQ ID NO 1; 130pp; English.
PS	
FX	The present invention provides hepatitis C virus (HCV) replication cells
CC	and cell lines derived from human non-hepatic cells or non-human cells..
CC	The inventions is useful for identifying anti-HCV agents for treating HCV
CC	infections. The present sequence is hepatitis C virus Con-1 replicon
CC	C1377/NS3-3' plasmid DNA.
XX	
SQ	Sequence 11313 BP; 2347 A; 3334 C; 3152 G; 2480 T; 0 U; 0 Other;
	Query Match 100.0%; Score 7990.4; DB 12; Length 11313;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GCCAGCCCCGATTGGGGCGACACTCCACCATAGTCACTCCCTGTGAGGAATACTG 60
Dd	1 GCCAGCCCCGATTGGGGCGACACTCCACCATAGTCACTCCCTGTGAGGAATACTG 60
QY	61 TCCTTCACGCAGAAACGGCTTAGCCATGGCGTTAGTATGAGTGTCGTGAGCCTCCAGGAC 120
Dd	61 TCCTTCACGCAGAAACGGCTTAGCCATGGCGTTAGTATGAGTGTCGTGAGCCTCCAGGAC 120
QY	121 CCCCGCTCCGGGAGAGCATAGTGCTTCGGGACCGGTGAGTACACCGGAATTGCCAG 180
Dd	121 CCCCGCTCCGGGAGAGCATAGTGCTTCGGGACCGGTGAGTACACCGGAATTGCCAG 180
QY	181 GAGCACGGGTCCTTCTTGAGTCAAACCGCTCAATGCTGGAGATTTGGCGTGC0CCC 240
Dd	181 GAGCACGGGTCCTTCTTGAGTCAAACCGCTCAATGCTGGAGATTTGGCGTGC0CCC 240
QY	241 GCGAGACTGCTAGCCGAGTAGTGTGGGTTCGGAAAGGCTTGCGTACTGCCGTATAGG 300
Dd	241 GCGAGACTGCTAGCCGAGTAGTGTGGGTTCGGGTCGGGAAAGGCTTGCGTACTGCCGTATAGG 300
QY	301 GTGCTTGCAGTGGCCCGGAGGTCTCGTAGACCGTGACCATGAGCAGAATCTTAAC 360
Dd	301 GTGCTTGCAGTGGCCCGGAGGTCTCGTAGACCGTGACCATGAGCAGAATCTTAAC 360
QY	361 CTCAAGAAAAACCAAAGCGCGCCATCATTTGAACAAGATGGATTGACGAGGTTCTC 420
Dd	361 CTCAAGAAAAACCAAAGCGCGCCATCATTTGAACAAGATGGATTGACGAGGTTCTC 420
QY	421 CGCGCGTTGGGTGGAGAGCTATTCCGCTATGACTGGGCACAACAGACAATCGCTGCT 480
Dd	421 CGCGCGTTGGGTGGAGAGCTATTCCGCTATGACTGGGCACAACAGACAATCGCTGCT 480
QY	481 CTGATGCGCGGTGTTCCGGCTCTCAGCGCAGGGGCGCCGGTTCCTTTTGTCAAGACGG 540
Dd	481 CTGATGCGCGGTGTTCCGGCTCTCAGCGCAGGGGCGCCGGTTCCTTTTGTCAAGACGG 540
QY	541 ACCTGTCCGTTGCCCTGAATGAATGAACTGACGAGCAGGAGCGCGGCTATCGTGGCTGCCA 600
Dd	541 ACCTGTCCGTTGCCCTGAATGAATGAACTGACGAGCAGGAGCGCGGCTATCGTGGCTGCCA 600
QY	601 CGAGCGGCGTTCTTTCGCGAGCTGTGCTCGACGTTGTCTACTGAAGCGGGAAGGGAATGGC 660
Dd	601 CGAGCGGCGTTCTTTCGCGAGCTGTGCTCGACGTTGTCTACTGAAGCGGGAAGGGAATGGC 660
QY	661 TGCTATTGGGCGAAGTGC0GGGGCAGGATCTCCTGTGTCATCTCAGCTTGTCTGCGCAGA 720
Dd	661 TGCTATTGGGCGAAGTGC0GGGGCAGGATCTCCTGTGTCATCTCAGCTTGTCTGCGCAGA 720
QY	721 AAGTATCCATCATGCTGATCAANTCGGGGCTGCAATCGCTTGATCCGGCTACCTGGC 780
Dd	721 AAGTATCCATCATGCTGATCAANTCGGGGCTGCAATCGCTTGATCCGGCTACCTGGC 780

1861 AGCCTCACAGGCGGACAGGAAACAGGTGCGAGGGGAGGTCCAAAGTGTCTCCACGGCA 1920 QY
1861 AGCCTCACAGGCGGACAGGAAACAGGTGCGAGGGGAGGTCCAAAGTGTCTCCACGGCA 1920 Db
1921 ACACAACTCTTTCTGCGGACCTGCGTCAATGGCGTGTGGAGTGTCTATCATGTGTGCC 1980 QY
1921 ACACAACTCTTTCTGCGGACCTGCGTCAATGGCGTGTGGAGTGTCTATCATGTGTGCC 1980 Db
1981 GGGTCAAGACGCTTGCAGGCGGCAAGGCGCAATCACCCAAATGTACACCAATGTGGAC 2040 QY
1981 GGGTCAAGACGCTTGCAGGCGGCAAGGCGCAATCACCCAAATGTACACCAATGTGGAC 2040 Db
2041 CAGGACCTCGTGGCGTGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100 QY
2041 CAGGACCTCGTGGCGTGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100 Db
2101 GGCAGCTCGGACCTTTACTTGTGTCAGAGGCGATGCCGATGTCATTCGGGTGCGCGGCGG 2160 QY
2101 GGCAGCTCGGACCTTTACTTGTGTCAGAGGCGATGCCGATGTCATTCGGGTGCGCGGCGG 2160 Db
2161 GGCAGCAGCAGGCGGAGCCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAGGCTCTTCG 2220 QY
2161 GGCAGCAGCAGGCGGAGCCTACTCTCCCGCAGGCGCGTCTCTACTTTGAAGGCTCTTCG 2220 Db
2221 GGCAGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTCCCGGTGTC 2280 QY
2221 GGCAGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTCCCGGTGTC 2280 Db
2281 ACCCGAGGGGTTGCGAAGCGGTGGACTTTGTACCGTCGAGTCTATGGAACCACTATG 2340 QY
2281 ACCCGAGGGGTTGCGAAGCGGTGGACTTTGTACCGTCGAGTCTATGGAACCACTATG 2340 Db
2341 CGGTCCCGGCTTTCACGAGCAACTCGTCCCTCGGCGCGTACCAGAGACATTTCCAGGTG 2400 QY
2341 CGGTCCCGGCTTTCACGAGCAACTCGTCCCTCGGCGCGTACCAGAGACATTTCCAGGTG 2400 Db
2401 GCCCATCTACAGGCGGCTTACTGTTAGCGGCAAGAGCACTAAGGTCCCGGCTCGGTATGCA 2460 QY
2401 GCCCATCTACAGGCGGCTTACTGTTAGCGGCAAGAGCACTAAGGTCCCGGCTCGGTATGCA 2460 Db
2461 GCCCAAGGGTATAGGTGCTTGTCTGAACCGCTCGGCGCGGCGGCGGCGGCGGCGGCGG 2520 QY
2461 GCCCAAGGGTATAGGTGCTTGTCTGAACCGCTCGGCGCGGCGGCGGCGGCGGCGGCGG 2520 Db
2521 GCGTATATGTTAAGGCACTGTTATGACCTTACATCAGAACCGGGGTAAAGACCATC 2580 QY
2521 GCGTATATGTTAAGGCACTGTTATGACCTTACATCAGAACCGGGGTAAAGACCATC 2580 Db
2581 ACCACGGGTGCCCATCAGCTACTCCACCTTATGGCAAGTTCCTTGGCGAGGTGTGCG 2640 QY
2581 ACCACGGGTGCCCATCAGCTACTCCACCTTATGGCAAGTTCCTTGGCGAGGTGTGCG 2640 Db
2641 TCTGGGCGGCTATGACATCATATATGTGATGATGCGCACTCACTCACTGACCTGACCACT 2700 QY
2641 TCTGGGCGGCTATGACATCATATATGTGATGATGCGCACTCACTCACTGACCTGACCACT 2700 Db
2701 ATCTGGGCATCGGCAAGTCTTGGCAAGCGGAGAGCGGTGGAGCGGCGGCGGCGGCGGCGG 2760 QY
2701 ATCTGGGCATCGGCAAGTCTTGGCAAGCGGAGAGCGGTGGAGCGGCGGCGGCGGCGGCGG 2760 Db
2761 CTGCGCACCGCTAGCGCTCGGGATCGGTACCGTGGCCACATCCAAACATCGAGGAGGTG 2820 QY
2761 CTGCGCACCGCTAGCGCTCGGGATCGGTACCGTGGCCACATCCAAACATCGAGGAGGTG 2820 Db
2821 GCTGTCTCAGCACTGGAGAAATCCCTTTTATGGCAAGCGGCGGCGGCGGCGGCGGCGGCGG 2880 QY
2821 GCTGTCTCAGCACTGGAGAAATCCCTTTTATGGCAAGCGGCGGCGGCGGCGGCGGCGGCGG 2880 Db
2881 AAGGGGGGAGGCACTCATTTTCTGCCATTTCCAAAGAAATGTGATGAGCTCGCGCGG 2940 QY
2881 AAGGGGGGAGGCACTCATTTTCTGCCATTTCCAAAGAAATGTGATGAGCTCGCGCGG 2940 Db
2941 AAGCTGTCCGCGCTCGGACCAATGTGTAGCATATTTACCGGGGCGGTTGATGTATCGGTC 3000 QY

2941 AAGCTGTCCGCGCTCGGACCTCAATGTGTAGCATATTTACCGGGGCGGTTGATGTATCGGTC 3000 Db
3001 ATACCAACTAGCGGAGACGTCATTTGTGTAGCAACGAGCGCTCTAATGACGGGCTTTACC 3060 QY
3001 ATACCAACTAGCGGAGACGTCATTTGTGTAGCAACGAGCGCTCTAATGACGGGCTTTACC 3060 Db
3061 GCGGATTTGCACTCACTGATCGACTGCAATATCATGTGTCAACGAGACAGTCGACTTTCAGC 3120 QY
3061 GCGGATTTGCACTCACTGATCGACTGCAATATCATGTGTCAACGAGACAGTCGACTTTCAGC 3120 Db
3121 CTGGACCCGACCTTACCAATTTGAGACGACGCGTCCCAACGAGCGGCTGTCAACGCTCG 3180 QY
3121 CTGGACCCGACCTTACCAATTTGAGACGACGCGTCCCAACGAGCGGCTGTCAACGCTCG 3180 Db
3181 CAGCGGCGAGGAGGAGCTGTTAGGGGCGAGATGGGCAITTTACAGGTTTGTGATCTCCAGGA 3240 QY
3181 CAGCGGCGAGGAGGAGCTGTTAGGGGCGAGATGGGCAITTTACAGGTTTGTGATCTCCAGGA 3240 Db
3241 GAACGGGCTCGGGCATGTTTCCATTTCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT 3300 QY
3241 GAACGGGCTCGGGCATGTTTCCATTTCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT 3300 Db
3301 GCTTGTGTACGAGCTCACGCGCGCGGAGACCTCAGTTAGTTTCTGGGAGGCTTACCTAAACACA 3360 QY
3301 GCTTGTGTACGAGCTCACGCGCGCGGAGACCTCAGTTAGTTTCTGGGAGGCTTACCTAAACACA 3360 Db
3361 CCAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGGCTTCTTACAGGCTTC 3420 QY
3361 CCAGGGTTGCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGGCTTCTTACAGGCTTC 3420 Db
3421 ACCCATAGAGCGGCGGCTTCTTGTCCAGACTAAGAGGCGAGGAGCAACTTCCCTTAC 3480 QY
3421 ACCCATAGAGCGGCGGCTTCTTGTCCAGACTAAGAGGCGAGGAGCAACTTCCCTTAC 3480 Db
3481 CTGTGTAGCATACAGGCTACGCGTACGCGGCTCAGGCTCAGCTTCCATCTCGTGGGAC 3540 QY
3481 CTGTGTAGCATACAGGCTACGCGTACGCGGCTCAGGCTCAGCTTCCATCTCGTGGGAC 3540 Db
3541 CAAATGTGGAAGTGTCTCATACGCTAAAGCTTACGCTGACGCGGCGGCGGCGGCGGCTG 3600 QY
3541 CAAATGTGGAAGTGTCTCATACGCTAAAGCTTACGCTGACGCGGCGGCGGCGGCGGCTG 3600 Db
3601 TATAGGCTGGGAGCGGCTTCAAAACGAGTTTACTACACACACCCCATAAACCAAAATACATC 3660 QY
3601 TATAGGCTGGGAGCGGCTTCAAAACGAGTTTACTACACACACCCCATAAACCAAAATACATC 3660 Db
3661 ATGGCATCATGTCTCGGCTGACCTGAGGTCTCAGGACCTTGGTGTCTGGTGGGCGG 3720 QY
3661 ATGGCATCATGTCTCGGCTGACCTGAGGTCTCAGGACCTTGGTGTCTGGTGGGCGG 3720 Db
3721 GTCCTAGGAGCTTGGCGCGGATTTGCTGACAAACAGGCGAGCTGCTTGTGGGCGG 3780 QY
3721 GTCCTAGGAGCTTGGCGCGGATTTGCTGACAAACAGGCGAGCTGCTTGTGGGCGG 3780 Db
3781 ATCATCTTGTCCGAAAGCGGCGGCTTCCGAGAGGGAAGTCTTTTACCGGAGTTC 3840 QY
3781 ATCATCTTGTCCGAAAGCGGCGGCTTCCGAGAGGGAAGTCTTTTACCGGAGTTC 3840 Db
3841 GATGAGATGGAAGAGTTCGCTCAGCTTCCCTTACATCGAAGGGAAGTCTTTTACCGGAGTTC 3900 QY
3841 GATGAGATGGAAGAGTTCGCTCAGCTTCCCTTACATCGAAGGGAAGTCTTTTACCGGAGTTC 3900 Db
3901 GAACAAATTTAAACAGAGGCAATCGGGTGTCTGCAACAGCCACCAAGAGGAGGCT 3960 QY
3901 GAACAAATTTAAACAGAGGCAATCGGGTGTCTGCAACAGCCACCAAGAGGAGGCT 3960 Db
3961 GCTGTCTCCGTGTGGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGGGCGGAGCATATG 4020 QY
3961 GCTGTCTCCGTGTGGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGGGCGGAGCATATG 4020 Db
4021 TGGAAATTTATCAGCGGATACATATTTAGAGGCTTGTCTCACTCTGCTCTGGGCAACCC 4080 QY

Db	4021	TGGAATTTTCATCAGCGGGATCAATATATTTAGCAGCTTGTCCACTCTGCTTGGCAACCCC	4080
QY	4081	GGGATAGCATCACTGATGSCATTTACAGCTCTATATCACACGCGCGCTCACACCAACAT	4140
Db	4081	GGGATAGCATCACTGATGSCATTTACAGCTCTATATCACACGCGCGCTCACACCAACAT	4140
QY	4141	ACCCTCCTGTTTAAACATCTCTGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGCT	4200
Db	4141	ACCCTCCTGTTTAAACATCTCTGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGCT	4200
QY	4201	GCTTCTGCTTTCTGATGGCGCGGCATCGCTGAGCGGCTGTGTGGCAGCATAGGCTTTGGG	4260
Db	4201	GCTTCTGCTTTCTGATGGCGCGGCATCGCTGAGCGGCTGTGTGGCAGCATAGGCTTTGGG	4260
QY	4261	ARGGTCTGTGGATATTTTGGCAGGTTATGAGCAGGGTGGCAGGCGCGCTCGTGGCC	4320
Db	4261	ARGGTCTGTGGATATTTTGGCAGGTTATGAGCAGGGTGGCAGGCGCGCTCGTGGCC	4320
QY	4321	TTTAAAGGTCAATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT	4380
Db	4321	TTTAAAGGTCAATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT	4380
QY	4381	ATCCTCTCCCTCGGCGCCCTAGTCTGTGCGGCTCGTGTGCGCAGCATACTGCTCGGCAC	4440
Db	4381	ATCCTCTCCCTCGGCGCCCTAGTCTGTGCGGCTCGTGTGCGCAGCATACTGCTCGGCAC	4440
QY	4441	GTGGGCCACGGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTGCTTTCGCGG	4500
Db	4441	GTGGGCCACGGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTGCTTTCGCGG	4500
QY	4501	GGTAAACACAGTCTCCCCCAGCCTATGTGCTGTGAGCGACGCTGACAGCGTGTCACT	4560
Db	4501	GGTAAACACAGTCTCCCCCAGCCTATGTGCTGTGAGCGACGCTGACAGCGTGTCACT	4560
QY	4561	CAGATCCTCTCTAGTCTTACATCACTCAGCTCTGAGAGGCTTCACCAGTGGATCAAC	4620
Db	4561	CAGATCCTCTCTAGTCTTACATCACTCAGCTCTGAGAGGCTTCACCAGTGGATCAAC	4620
QY	4621	GAGACTGTCTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGGATATGC	4680
Db	4621	GAGACTGTCTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTTGGATATGC	4680
QY	4681	ACGGTGTGTAGTGAATTTCAAGACTGTGGCTCAGTCCMAAGCTCTTGGCGGATTCGGGA	4740
Db	4681	ACGGTGTGTAGTGAATTTCAAGACTGTGGCTCAGTCCMAAGCTCTTGGCGGATTCGGGA	4740
QY	4741	GTCCCTCTTCTCATGTCAAGTGGGTACAGAGGAGTCTGGCGGGCGACGSCATCATG	4800
Db	4741	GTCCCTCTTCTCATGTCAAGTGGGTACAGAGGAGTCTGGCGGGCGACGSCATCATG	4800
QY	4801	CAAAACCACTGCGCATGTGGAGCACAGATCACCGGACATGTGAAAACGGTTCCTATGAG	4860
Db	4801	CAAAACCACTGCGCATGTGGAGCACAGATCACCGGACATGTGAAAACGGTTCCTATGAG	4860
QY	4861	ATCGTGGGGCCTPAGGACCTGTAGTAAACAGTGGGATGGAACANTTCCCATTTACGGGTAC	4920
Db	4861	ATCGTGGGGCCTPAGGACCTGTAGTAAACAGTGGGATGGAACANTTCCCATTTACGGGTAC	4920
QY	4921	ACCAAGGGCCCTGCACGCCCTCCCGCGCCAAATTTACTAGGGCGCTGTGGCGGGTG	4980
Db	4921	ACCAAGGGCCCTGCACGCCCTCCCGCGCCAAATTTACTAGGGCGCTGTGGCGGGTG	4980
QY	4981	GCTGCTGAGGAGTACGTGTGAGGTTTACGCGGGTGGGGATTTCCACTACGTGACGGGCATG	5040
Db	4981	GCTGCTGAGGAGTACGTGTGAGGTTTACGCGGGTGGGGATTTCCACTACGTGACGGGCATG	5040
QY	5041	ACCACGTGACAAAGTAAAGTGCCCGTGTAGGTTTCGGCCCCCGAAATTTCTTTCACAGAGTG	5100
Db	5041	ACCACGTGACAAAGTAAAGTGCCCGTGTAGGTTTCGGCCCCCGAAATTTCTTTCACAGAGTG	5100
QY	5101	GATGGGGTGGGTGTGACAGGTACGCTTCAGCGTGCAAAACCCCTCTCTACGGGAGAGGTC	5160
Db	5101	GATGGGGTGGGTGTGACAGGTACGCTTCAGCGTGCAAAACCCCTCTCTACGGGAGAGGTC	5160

5161	A	C	A	T	T	C	T	G	G	T	C	A	A	T	A	C	T	G	T	T	G	G	T	C	A	C	A	G	T	C	C	C	A	T	G	C	G	A		5220			
5161	A	C	A	T	T	C	T	G	T	C	G	G	T	C	A	A	T	A	C	T	G	T	T	G	G	T	C	A	C	A	G	T	C	C	C	A	T	G	C	G	A		5220
5221	C	G	G	A	C	G	T	A	G	C	A	G	T	C	A	T	T	C	C	A	T	G	T	C	A	C	C	C	C	T	C	C	C	A	T	T	A	C	G	G	A		5280
5221	C	G	G	A	C	G	T	A	G	C	A	G	T	C	A	T	T	C	C	A	T	G	T	C	A	C	C	C	C	C	T	C	C	A	T	T	A	C	G	G	A		5280
5281	G	C	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		5340			
5281	G	C	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		5340				
5341	C	T	G	T	C	G	C	C	T	T	C	T	T	G	A	A	G	C	A	T	G	A	A	G	C	A	T	G	A	A	G	C	A	T	G	A	A	G		5400			
5341	C	T	G	T	C	G	C	C	T	T	C	T	T	G	A	A	G	C	A	T	G	A	A	G	C	A	T	G	A	A	G	C	A	T	G	A	A	G		5400			
5401	C	T	C	A	T	C	A	G	G	C	C	A	A	C	T	C	T	G	G	C	G	C	A	G	A	G	A	T	C	C	T	G	G	C	G	A	A	C	A		5460		
5401	C	T	C	A	T	C	A	G	G	C	C	A	A	C	T	C	T	G	G	C	G	C	A	G	A	G	A	T	C	C	T	G	G	C	G	A	A	C	A		5460		
5461	T	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		5520				
5461	T	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		5520				
5521	A	G	G	A	G	A	T	C	C	T	C	C	G	C	G	A	G	A	T	C	C	G	C	G	A	G	A	T	C	C	G	C	G	A	A	A	A	A	A		5580		
5521	A	G	G	A	G	A	T	C	C	T	C	C	G	C	G	A	G	A	T	C	C	G	C	G	A	G	A	T	C	C	G	C	G	A	A	A	A	A	A		5580		
5581	C	C	C	A	T	A	T	G	G	C	A	C	C	T	C	C	A	C	T	G	T	T	A	G	A	T	C	C	T	G	A	G	A	G	A	C	C	G	A		5640		
5581	C	C	C	A	T	A	T	G	G	C	A	C	C	T	C	C	A	C	T	G	T	T	A	G	A	T	C	C	T	G	A	G	A	G	A	C	C	G	A		5640		
5641	T	A	C	T	C	C	T	C	A	G	G	T	G	C	A	T	T	C	C	G	C	C	T	G	C	A	T	T	C	C	G	A	A	C	C	C	C	C	A		5700		
5641	T	A	C	T	C	C	T	C	A	G	G	T	G	C	A	T	T	C	C	G	C	C	T	G	C	A	T	T	C	C	G	A	A	C	C	C	C	C	A		5700		
5701	C	C	T	C	A	C	G	A	G	A	G	A	G	A	G	A	G	A	T	C	A	G	A	T	C																		

Db 1681 ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTAGTCGAGGTTAAAA 1740
Qy 1741 AACGTCATAGGCCCCCGAACCACAGGGGACGTGGTTTTCCTTTTCGAAAAACACGATATACC 1800
Db 1741 AACGTCATAGGCCCCCGAACCACAGGGGACGTGGTTTTCCTTTTCGAAAAACACGATATACC 1800
Qy 1801 ATGGCGCCTATTACGGCTTACTCCCAACAGACGCGAGGCTACTTGGCTGCAATCACT 1860
Db 1801 ATGGCGCCTATTACGGCTTACTCCCAACAGACGCGAGGCTACTTGGCTGCAATCACT 1860
Qy 1861 AGCCTCACAGGCGGGACAGGAACACAGGTCCGAGGGGGAGTCCAAAGTGTCTCCACCGCA 1920
Db 1861 AGCCTCACAGGCGGGACAGGAACACAGGTCCGAGGGGGAGTCCAAAGTGTCTCCACCGCA 1920
Qy 1921 ACAAAATCTTCTGGCGACCTGCGTCAATGGGGTGTGGTCTCTATCATGTTGCC 1980
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Db 3841 GATCAGATGGAAGTGCCTCACCTCCCTTACATCGAAACAGGGAATCAGCTCGCC 3900

PH Key Location/Qualifiers
FT CDS 1801..7759
FT /*tag= a
FT /product= "HCV replicon"
XX WO2004015131-A2.
XX 19-FEB-2004.
XX 12-AUG-2003; 2003WO-US025260.
XX 12-AUG-2002; 2002US-0402661P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Gao M, Lemm JA, O'boyle DR, Nower P, Rigat K, Sun J;
XX WPI; 2004-180685/17.
XX P-PSDB; ADJ57846.
XX Use of hepatitis C virus assays or reporter assays, e.g. identifying a
XX compound that inhibits hepatitis C virus RNA replication or identifying a
XX compound that modulates the activity of a gene of interest.
XX Claim 3; SEQ ID NO 1; 45pp; English.
XX
XX The present invention relates to the use of hepatitis C virus (HCV)
XX assays for identifying a compound that inhibits HCV RNA replication and
XX reporter assays for identifying a compound that modulates the activity of
XX a gene of interest. The assays are useful for identifying a compound that
XX inhibits HCV RNA replication or for identifying a compound that modulates
XX the activity of a gene of interest. The HCV assay is useful for high
XX throughput screening that quantifies both the amount of HCV RNA
XX replication inhibitory activity associated with a test compound and the
XX amount of cytotoxicity associated with the test compound. The compound is
XX useful for treating hepatitis C infection. Assays of the invention have
XX distinct advantages when compared to qRT-PCR or other methods in that
XX assays of the invention may take place in situ in a detergent based crude
XX cell lysate, which requires no further preparation prior to performing
XX the assays. The assays do not also involve numerous manipulations to add
XX or subtract reagents after addition of test compounds and are desirably
XX based on a viral protein which is required by the HCV replicon for
XX replication. The present sequence represents a HCV replicon encoding
XX sequence used in the assay of the invention.
SQ Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;
Query Match 100.0%; Score 7989; DB 12; Length 7989;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTGTG 60
DB 1 GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTGTG 60
QY 61 TCTTCACGACGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGAGCCTCCAGGAC 120
DB 61 TCTTCACGACGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGAGCCTCCAGGAC 120
QY 121 CCCCCCTCCGGGAGAGCATTAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
DB 121 CCCCCCTCCGGGAGAGCATTAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
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DB 181 GACGACCGGTCTCTTTCTTGGATCAACCGCTCAATGCTGGAGATTGGGGGTCCCC 240
QY 241 GCGAGACTCTAGCCGAGTAGTGTGGTTCGCGAAAGGCTTTGTGCTACTGCTGATAGG 300
DB 241 GCGAGACTCTAGCCGAGTAGTGTGGTTCGCGAAAGGCTTTGTGCTACTGCTGATAGG 300
QY 301 GTGCTTGGAGTCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
DB 301 GTGCTTGGAGTCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360

DB 301 GTGCTTGGAGTCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
QY 361 CTCAAGAGAAAACCAAGGGCGGCCCATGATTGAACAAGATGAGATTGCACGACGTTCTC 420
DB 361 CTCAAGAGAAAACCAAGGGCGGCCCATGATTGAACAAGATGAGATTGCACGACGTTCTC 420
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QY 481 CTGATGCGCGCTGTTCCGGCTGTGAGGAGGCGCGCGGCTGTTCTTTTTCAGACCG 540
DB 481 CTGATGCGCGCTGTTCCGGCTGTGAGGAGGCGCGCGGCTGTTCTTTTTCAGACCG 540
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DB 841 TTGTGATCAGATGATCTGACGAGAGGATCAGGGGCTCGCGCAGCGGAGGAGGAGGAGG 900
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Qy	3661	ATGGCATGATGTCGGTACCTGGAGGTGCTCAAGAGACCTGGGTGCTGGTAGCGGA	3720	Qy	4741	GTCCCTCTTCTTCATGTCAACGTCGCTCAAGAGGAGTCTGGCGGGCGACAGCATCATG	4800
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Qy	3721	GTCTAGCAGCTTGGCGCGGTATGCTGACACAGGAGCGTGTCTATTTGGGCGAGG	3780	Qy	4801	CAAAACACCTGCCCATGTGGAGCACAGATCAACCGGACATGTGAATAACCGTTCCATGAGG	4860
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Qy	3781	ATCATCTTGTCCGAAAGCCGGCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC	3840	Qy	4861	ATCGTGGGGCTTAGGACCTGTAGTAACAGCTGGCATGGAACATTTCCCATTAACGGGTAC	4920
Db	3781	ATCATCTTGTCCGAAAGCCGGCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC	3840	Db	4861	ATCGTGGGGCTTAGGACCTGTAGTAACAGCTGGCATGGAACATTTCCCATTAACGGGTAC	4920
Qy	3841	GATGAGATGAAGTGGCTTACACCTCCCTTACATCGAAGGGAATGCACTCGCC	3900	Qy	4921	ACCACGGGCCCTCGACCGCTCCCGGGCCCAAAATTAATTTCTAGGGCGCTGTGGCGGGTG	4980
Db	3841	GATGAGATGAAGTGGCTTACACCTCCCTTACATCGAAGGGAATGCACTCGCC	3900	Db	4921	ACCACGGGCCCTCGACCGCTCCCGGGCCCAAAATTAATTTCTAGGGCGCTGTGGCGGGTG	4980
Qy	3901	GAACAAATTCAGAGGCAATCGGGTTGCTGCAACAGCCACCAAGCAAGCGGAGCT	3960	Qy	4981	GCTGCTGAGGAGTACGTGGAGGTTACGCGGGTGGGGATTTCCACTACGTGAACGGGATG	5040
Db	3901	GAACAAATTCAGAGGCAATCGGGTTGCTGCAACAGCCACCAAGCAAGCGGAGCT	3960	Db	4981	GCTGCTGAGGAGTACGTGGAGGTTACGCGGGTGGGGATTTCCACTACGTGAACGGGATG	5040
Qy	3961	GCTGCTCCGCTGGTGAATCCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG	4020	Qy	5041	ACCACTACAAACGTAAAGTCCCGTGTCAAGTTCGGGCCCGCAATTTCTTCAAGAAAGTG	5100
Db	3961	GCTGCTCCGCTGGTGAATCCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG	4020	Db	5041	ACCACTACAAACGTAAAGTCCCGTGTCAAGTTCGGGCCCGCAATTTCTTCAAGAAAGTG	5100
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Qy	4081	GCGATAGCATCACTGATGGCAATTCACAGCTCTATCACCAGCCGCTCAACCCCAACAT	4140	Qy	5161	ACATTTCTGGTTCGGGCTCAATCAATACCTGTTGGGTCAAGCTCCCATGCGAGCCCGAA	5220
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Qy	4141	ACCTCTCTGTTTAAATCTCTGGGGGATGCGTGGCGGCGCCCAACTTGTCTCCAGCGCT	4200	Qy	5221	CCGACGTAGCAGTGTCTTCCATGCTCACCAGCCCTCCACATTTAGCGCGAGACG	5280
Db	4141	ACCTCTCTGTTTAAATCTCTGGGGGATGCGTGGCGGCGCCCAACTTGTCTCCAGCGCT	4200	Db	5221	CCGACGTAGCAGTGTCTTCCATGCTCACCAGCCCTCCACATTTAGCGCGAGACG	5280
Qy	4201	GCTTCTGCTTTCGAGGCGCGGATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTGGG	4260	Qy	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTAGCCAG	5340
Db	4201	GCTTCTGCTTTCGAGGCGCGGATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTGGG	4260	Db	5281	GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTAGCCAG	5340
Qy	4261	AAGTGTCTTGGGATATTTGGCAGGTTATGGAGCGGCTGTCAGCGGCTGCTGGCC	4320	Qy	5341	CTGTCTGGCTTCTTTGAAAGCAATGACATACCTGCTATGACTCCCGGAGCTGAC	5400
Db	4261	AAGTGTCTTGGGATATTTGGCAGGTTATGGAGCGGCTGTCAGCGGCTGCTGGCC	4320	Db	5341	CTGTCTGGCTTCTTTGAAAGCAATGACATACCTGCTATGACTCCCGGAGCTGAC	5400
Qy	4321	TTTAAGGTTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT	4380	Qy	5401	CTCATCGAGCCACCTCTCTGCGCGAGAGATGGCGGGAACATCACCCTGCTGGAG	5460
Db	4321	TTTAAGGTTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT	4380	Db	5401	CTCATCGAGCCACCTCTCTGCGCGAGAGATGGCGGGAACATCACCCTGCTGGAG	5460
Qy	4381	ATCCTCTCCCTGGGCCCTAGTGTGGGTGCTGGCGAGCATACTGCTGGCAC	4440	Qy	5461	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTTCAGCGCTCCAAAGCGGAGGATGAG	5520
Db	4381	ATCCTCTCCCTGGGCCCTAGTGTGGGTGCTGGCGAGCATACTGCTGGCAC	4440	Db	5461	TCAGAAATTAAGGTAGTAAATTTTGGACTCTTTTCAGCGCTCCAAAGCGGAGGATGAG	5520
Qy	4441	GTGGGCCAGAGGAGGCGCTGTGAGTGAATGAACCGGCTGATAGCGCTTGGCGG	4500	Qy	5521	AGGAAATATCCGTTCCGCGGAGATCTCTGCGGAGGTCAGGAAATTTCCCTCGAGCGATG	5580
Db	4441	GTGGGCCAGAGGAGGCGCTGTGAGTGAATGAACCGGCTGATAGCGCTTGGCGG	4500	Db	5521	AGGAAATATCCGTTCCGCGGAGATCTCTGCGGAGGTCAGGAAATTTCCCTCGAGCGATG	5580
Qy	4501	GGTAACACAGTCTCCCGCAGCATATGTGCTGAGAGCGAGCTGTGAGCGTGTCACT	4560	Qy	5581	CCCATATGGGCACCGCGGATTTACAAACCTCTTGTAGAGTCTGTAAGAGGACCCGGAC	5640
Db	4501	GGTAACACAGTCTCCCGCAGCATATGTGCTGAGAGCGAGCTGTGAGCGTGTCACT	4560	Db	5581	CCCATATGGGCACCGCGGATTTACAAACCTCTTGTAGAGTCTGTAAGAGGACCCGGAC	5640
Qy	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGCTTCCACAGTGAATCAAC	4620	Qy	5641	TACGTCCCTCCAGTGGTACACGGGTGTCCATTTGCGCTGCGCAAGGCGCTCCCATACCA	5700
Db	4561	CAGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGCTTCCACAGTGAATCAAC	4620	Db	5641	TACGTCCCTCCAGTGGTACACGGGTGTCCATTTGCGCTGCGCAAGGCGCTCCCATACCA	5700
Qy	4621	GAGGACTGCTCCACGCCATGCTCCCGCTCGTGGCTAAGAGATGTTTGGGATTTGATGTC	4680	Qy	5701	GCTCCAGGAGAGAGACGGTGTCTGTGAGAAATCTACCGTGTCTTCTGCTTGGCG	5760
Db	4621	GAGGACTGCTCCACGCCATGCTCCCGCTCGTGGCTAAGAGATGTTTGGGATTTGATGTC	4680	Db	5701	GCTCCAGGAGAGAGACGGTGTCTGTGAGAAATCTACCGTGTCTTCTGCTTGGCG	5760
Qy	4681	ACGGTGTGATGATTTTAAGACCTGGGCTCAGTCCAAAGCTCTGCGCGGATTTCCCGGA	4740	Qy	5761	GAGCTCGGCACAAAGACCTTCGGCAGCTCCGAAATCGTGGCGCTCGACAGCGGACGGA	5820
Db	4681	ACGGTGTGATGATTTTAAGACCTGGGCTCAGTCCAAAGCTCTGCGCGGATTTCCCGGA	4740	Db	5761	GAGCTCGGCACAAAGACCTTCGGCAGCTCCGAAATCGTGGCGCTCGACAGCGGACGGA	5820

Db 7981 AGATCAAGT 7989

RESULT 13
ABK91440
ID ABK91440 standard; DNA; 10690 BP.

XX
AC ABK91440;
XX
DT 15-NOV-2002 (first entry)
XX
DE Hepatitis C virus vector construct pHCVNeo.17m7.
XX
KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
XX internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX
OS Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.

XX Key Location/Qualifiers
FT 5'UTR 1..341
FT /*tag= a
FT CDS 342..1181
FT /*tag= b
FT /product= "Core-neo fusion protein"
FT /1190..1800
FT /*tag= c
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FT /note= "Internal ribosome entry site from ECMV"
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FT /*tag= d
FT /product= "Polyprotein"
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FT /*tag= e
FT mutation replace(5243,C)
FT /*tag= f
FT 3'UTR 7759..7791
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FT misc_feature 7792..10690
FT /*tag= h
FT /note= "Plasmid derived sequences"

PN WO200259321-A2.
XX
XX
PD 01-AUG-2002.
XX
PF 16-JAN-2002; 2002WO-EF000526.
XX
PR 23-JAN-2001; 2001US-0263479P.
XX
PA (RICE-) 1ST RICERHE BIOL MOLECOLARE ANGELETTI.
XX
PI De Francesco R, Migliaccio G, Paonessa G;
XX
DR WPI; 2002-599793/64.
XX
PT New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.
XX
PS Claim 16; Page; 69pp; English.
XX
CC The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations

QY 721 AAGTATCCATCATGGCTGATGCAATCGCGGGCTGATACGCTTGATCGGGCTACCTGCC 780
DB 721 AAGTATCCATCATGGCTGATGCAATCGCGGGCTGATACGCTTGATCGGGCTACCTGCC 780
QY 781 CATTCGACCAACAGGAAACATCGCATCGAGCGAGCAGTACTCGATCGAAGCCGGTCC 840
DB 781 CATTCGACCAACAGGAAACATCGCATCGAGCGAGCAGTACTCGAATCGAAGCCGGTCC 840
QY 841 TTGTGATCAGGATGATCTGACGAGAGAGCATCAGGGGCTCGCGCCAGCCGAACTCTTCC 900
DB 841 TTGTGATCAGGATGATCTGACGAGAGAGCATCAGGGGCTCGCGCCAGCCGAACTCTTCC 900
QY 901 CAGAGCTAAGCGGGGCGATGCGCGAGAGAGATCTCGTGTGACCCATGCGAGTGCCT 960
DB 901 CAGAGCTAAGCGGGGCGATGCGCGAGAGAGATCTCGTGTGACCCATGCGAGTGCCT 960
QY 961 GCTTGGCGAATATCATGTGTGAAATGCGCGCTTTCTGTGATTCATCGACTGTGGCGGC 1020
DB 961 GCTTGGCGAATATCATGTGTGAAATGCGCGCTTTCTGTGATTCATCGACTGTGGCGGC 1020
QY 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCCGTGCGTACCCGTGATATTGCTGAAGAGC 1080
DB 1021 TGGGTGTGGCGGACCGCTATCAGGACATAGCCGTGCGTACCCGTGATATTGCTGAAGAGC 1080
QY 1081 TTGGCGGGAATGGGCTGACCGCTTCTCGTGTGATTCGATATCGCTTCCCGATTGCG 1140
DB 1081 TTGGCGGGAATGGGCTGACCGCTTCTCGTGTGATTCGATATCGCTTCCCGATTGCG 1140
QY 1141 AGCGCATCGCCTTCTATCGCCTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
DB 1141 AGCGCATCGCCTTCTATCGCCTTCTGAGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
QY 1201 GTTCCCTCTAGCGGATCAATTCCGCGCTTCTCGCTTCTGATATCGCTTCCCGATTGCG 1260
DB 1201 GTTCCCTCTAGCGGATCAATTCCGCGCTTCTCGCTTCTGATATCGCTTCCCGATTGCG 1260
QY 1261 CGAAGCGCTTGGATTAAGCGCGGTGCGTGTGCTATATGTTATTTTCCACCATATTG 1320
DB 1261 CGAAGCGCTTGGATTAAGCGCGGTGCGTGTGCTATATGTTATTTTCCACCATATTG 1320
QY 1321 CCGTCTTTTGGCAATGTCAGGCGCCGGAACCTGCGCCTGCTTCTTACGAGCATTCCT 1380
DB 1321 CCGTCTTTTGGCAATGTCAGGCGCCGGAACCTGCGCCTGCTTCTTACGAGCATTCCT 1380
QY 1381 AGGGGTCTTCCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGCTGTAAGGAAGCA 1440
DB 1381 AGGGGTCTTCCCTCTCGCCAAAGGAATCAAGGTCTGTTGAATGCTGTAAGGAAGCA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGCTGTGAGCACCTTTGAGGAGCGG 1500
DB 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGCTGTGAGCACCTTTGAGGAGCGG 1500
QY 1501 AACCCCGCACCTGCGGACAGTGCCTCTGCGGCCAAAGCCACGCTGATAGATACACCT 1560
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QY 1561 GCAAAGCGGCACAAACCCAGTGCACGTTGTGAGTTGGATGTTGTGGAAGAGTCAAA 1620
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DB 1621 TGGCTCTCTCAAGCTATTCAACAGGGGCTGAAGGATGCCAGAGGTACCCCATTTGT 1680
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DB 1681 ATGGGATCTGATCTGGGGCTCGGTGACATGCTTTACATGTTGTTAGTCAGGTTAAAA 1740
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DB 1741 AACGTCTAGGCCCCCGAAACCAAGGAGCGGTGTTTCTTTTGAAGAACAGTAATACC 1800
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DB 1801 ATGGCGCTATTACGGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCACT 1860
QY 1861 AGCCTCACAGCGCGGACAGGAAACAGAGTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
DB 1861 AGCCTCACAGCGCGGACAGGAAACAGAGTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
QY 1921 ACACATCTTTCTGCGGACCTGCGTCAATGCGGTGTGTGGACTCTTATCATGTGTC 1980
DB 1921 ACACATCTTTCTGCGGACCTGCGTCAATGCGGTGTGTGGACTCTTATCATGTGTC 1980
QY 1981 GGTCAAAGACCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC 2040
DB 1981 GGTCAAAGACCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC 2040
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DB 2041 CAGGACCTGTCGCTGCGTCAAGCGCCCCCGGGGCGGTTCCTTGACACATGCACCTGC 2100
QY 2101 GGCAGCTCGGACCTTTACTTGTGTCAGAGGCAATGCGGATGTCAATTCGGTGTGCGCGG 2160
DB 2101 GGCAGCTCGGACCTTTACTTGTGTCAGAGGCAATGCGGATGTCAATTCGGTGTGCGCGG 2160
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DB 2161 GCGGACAGCAGGGGAGCGCTACTCTCCCCCAGGCGCGCTTCTTGAAGGGCTCTTGC 2220
QY 2221 GCGGTCCACTGCTCTGCGCCCTCGGGGCAAGCTGTGGGCACTTTTCGGGCTCCGCTGTC 2280
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DB 2281 ACCGAGGGGTTCGGAAGCGCGTGAATTTGTACCCGTCGAGTCTATGGAACCACTATG 2340
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DB 2341 CCGTCCCCCGTCTTCAAGCAAACTCGCTCCCTCGCGCGTACCGGCACTTTTCGGGCTCCGCTGTC 2400
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QY 2461 GCGCAAGGGTATAAGTGTCTGTGTAACCCGTCGCTGCGCGCAACCTAGGTTTCGG 2520
DB 2461 GCGCAAGGGTATAAGTGTCTGTGTAACCCGTCGCTGCGCGCAACCTAGGTTTCGG 2520
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DB 2521 GCGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACCGGGTAAAGCAATC 2580
QY 2581 ACCAGGGTCCCCCATCAAGTACTCCACCTATGCGCAAGTTTCTTTCGCGAGCGGTGTC 2640
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QY 2761 CTGCGCACCGCTACGCTCCCGGATCGGTCAAGTGCACATCAAAACATCGAGGAGGTG 2820
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QY 2821 GCTCTGTCCAGCATGAGGAAATCCCTTTTATGGAAGGCAATCCCATCGAGCAATC 2880
DB 2821 GCTCTGTCCAGCATGAGGAAATCCCTTTTATGGAAGGCAATCCCATCGAGCAATC 2880
QY 2881 AAGGGGGGAGGCACTCTTCTGCTTCTGCAATTCACAGAGAAATGTGATGAGTGCAGCGG 2940

Dd	2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCCAGAGAAATGTGATGAGCTCGCCGG	2940	4021	TGGAATTTTCATCAGCGGGATACAATATTATAGCAGGCTTGTCCACTCTGCTGGCAACCC	4080	
Qy	2941	AAGCTGTCCGGCTCGGACTCAATGTGTAGACATATTACGGGGCCCTTGATGTATCCGTC	3000	Dd	4021	TGGAATTTTCATCAGCGGGATACAATATTATAGCAGGCTTGTCCACTCTGCTGGCAACCC	4080
Dd	2941	AAGCTGTCCGGCTCGGACTCAATGTGTAGACATATTACGGGGCCCTTGATGTATCCGTC	3000	Qy	4081	GGATAGCATCATGTATGGCATTCAGAGCTCTATCACCAGCCGCTCACCACCCCAACAT	4140
Qy	3001	ATACCAACTAGCGGAGACGTCTATGTGTAGAACGGACGCTTAATAGCGGCTTTTACC	3060	Dd	4081	GGATAGCATCATGTATGGCATTCAGAGCTCTATCACCAGCCGCTCACCACCCCAACAT	4140
Dd	3001	ATACCAACTAGCGGAGACGTCTATGTGTAGAACGGACGCTTAATAGCGGCTTTTACC	3060	Qy	4141	ACCTCTCTTTTAAACATCTGGGGGATGGTGGCCGCCCAACTTGTCTCTCCAGCGCT	4200
Qy	3061	GGCGATTTCCAGTCACTGATCGACTGCAATACATGTGTACCAGACAGTCGACTTCAGC	3120	Dd	4141	ACCTCTCTTTTAAACATCTGGGGGATGGTGGCCGCCCAACTTGTCTCTCCAGCGCT	4200
Dd	3061	GGCGATTTCCAGTCACTGATCGACTGCAATACATGTGTACCAGACAGTCGACTTCAGC	3120	Qy	4201	GCTTCTGCTTTTGTAGCGCGGCATCTGCTGGAGCGGCTTGTGGCAGCATATGGCCTTGGG	4260
Qy	3121	CTGGACCCGACCTTCCATTTGAGACGACACCGTGGCCACAGACGGGCTGTCAGCTCG	3180	Dd	4201	GCTTCTGCTTTTGTAGCGCGGCATCTGCTGGAGCGGCTTGTGGCAGCATATGGCCTTGGG	4260
Dd	3121	CTGGACCCGACCTTCCATTTGAGACGACACCGTGGCCACAGACGGGCTGTCAGCTCG	3180	Qy	4261	AAGGTGCTGTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCTGTGGCC	4320
Qy	3181	CAGCGGAGGACGAGCTGTGTAGGGGAGGATGGCAATTTACAGGTTTGTGACTCCAGGA	3240	Dd	4261	AAGGTGCTGTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCTGTGGCC	4320
Dd	3181	CAGCGGAGGACGAGCTGTGTAGGGGAGGATGGCAATTTACAGGTTTGTGACTCCAGGA	3240	Qy	4321	TTTAAAGTCAATAGCGCGGCATGCCCTCCACCGAGACCTGTGTTAACTACTCTCTGCT	4380
Qy	3241	GAACGGCCCTCGGCAATTTTCTGCTTCTGCTGAGTGTCTATGACGCGGGCTGT	3300	Dd	4321	TTTAAAGTCAATAGCGCGGCATGCCCTCCACCGAGACCTGTGTTAACTACTCTCTGCT	4380
Dd	3241	GAACGGCCCTCGGCAATTTTCTGCTTCTGCTGAGTGTCTATGACGCGGGCTGT	3300	Qy	4381	ATCCTCTCCCTCGCGCCCTTAGTCTCGGGCTCGTGTGCGCAGCGATCTGCTGGCAC	4440
Qy	3301	GCTTGTACGAGTCAACCGCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA	3360	Dd	4381	ATCCTCTCCCTCGCGCCCTTAGTCTCGGGCTCGTGTGCGCAGCGATCTGCTGGCAC	4440
Dd	3301	GCTTGTACGAGTCAACCGCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA	3360	Qy	4441	GTGGCCCGAGGGAGGGGCTGTGATGATGAACCGGCTGTAGGCTTCCGCTTCGCGG	4500
Qy	3361	CCAGGTTGCCGCTCTGCGAGGACCATCTGAGTTCTGGGAGAGCGTCTTTACAGGCTC	3420	Dd	4441	GTGGCCCGAGGGAGGGGCTGTGATGATGAACCGGCTGTAGGCTTCCGCTTCGCGG	4500
Dd	3361	CCAGGTTGCCGCTCTGCGAGGACCATCTGAGTTCTGGGAGAGCGTCTTTACAGGCTC	3420	Qy	4501	GGTAAACACAGCTCTCCCGACGCACTATGTGCTGAGAGCGACGCTGACGACGCTGCT	4560
Qy	3421	ACCCACATAGACGCCCATTTCTTCTCCAGACTAAGCAGCAGGAGACAACTTCCCTTAC	3480	Dd	4501	GGTAAACACAGCTCTCCCGACGCACTATGTGCTGAGAGCGACGCTGACGACGCTGCT	4560
Dd	3421	ACCCACATAGACGCCCATTTCTTCTCCAGACTAAGCAGCAGGAGACAACTTCCCTTAC	3480	Qy	4561	CAGATCTCTCTAGTCTTACCATCACTAGTGTCTGAAGAGGCTTCAACAGTGTATCAAC	4620
Qy	3481	CTGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCAGCTCCACCTCCATCGTGGAC	3540	Dd	4561	CAGATCTCTCTAGTCTTACCATCACTAGTGTCTGAAGAGGCTTCAACAGTGTATCAAC	4620
Dd	3481	CTGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCAGCTCCACCTCCATCGTGGAC	3540	Qy	4621	GAGACTGTCTCAGCGCCATGCTCCGGCTGCTGAGATGTTTGGGATGGATATGC	4680
Qy	3541	CAATGTGGAGTGTCTCATAGGCTAAAGCTACGCTGACAGGCGCAACGCCCTCTGCTG	3600	Dd	4621	GAGACTGTCTCAGCGCCATGCTCCGGCTGCTGAGATGTTTGGGATGGATATGC	4680
Dd	3541	CAATGTGGAGTGTCTCATAGGCTAAAGCTACGCTGACAGGCGCAACGCCCTCTGCTG	3600	Qy	4681	ACGCTGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGCTCCTGCCCGGATGCGCGGA	4740
Qy	3601	TATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATAAACCAATACATC	3660	Dd	4681	ACGCTGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGCTCCTGCCCGGATGCGCGGA	4740
Dd	3601	TATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATAAACCAATACATC	3660	Qy	4741	GTCCCTTCTTCTCATGTCAAAGGGGTAAGGGAGTCTGGCGGGGCGAGGCGATCATG	4800
Qy	3661	ATGGCATGCATGTCCGCTGACCTGAGGTCTGTCAGAGCACTGGGTCTGTAGGCGGA	3720	Dd	4741	GTCCCTTCTTCTCATGTCAAAGGGGTAAGGGAGTCTGGCGGGGCGAGGCGATCATG	4800
Dd	3661	ATGGCATGCATGTCCGCTGACCTGAGGTCTGTCAGAGCACTGGGTCTGTAGGCGGA	3720	Qy	4801	CAAAACACCTGCCATGTGGAGCACAGATCACCGGACATGTGMAAAACGGTTCCATGAGG	4860
Qy	3721	GTCTAGCAGCTCTGCGCGGCTATTGCTGACACAGCAGCGGTGCTCATTTGGGCGAGG	3780	Dd	4801	CAAAACACCTGCCATGTGGAGCACAGATCACCGGACATGTGMAAAACGGTTCCATGAGG	4860
Dd	3721	GTCTAGCAGCTCTGCGCGGCTATTGCTGACACAGCAGCGGTGCTCATTTGGGCGAGG	3780	Qy	4861	ATCTGGGGCCCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGCTAC	4920
Qy	3781	ATCATCTTTTCCGAAAGCGCGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC	3840	Dd	4861	ATCTGGGGCCCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGCTAC	4920
Dd	3781	ATCATCTTTTCCGAAAGCGCGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC	3840	Qy	4921	ACCACGGGCCCCGTGACGCCCTTCCCGCGCCAAATTTATTAGGGCGCTGTGGCGGGTG	4980
Qy	3841	GATGAGATGGAGTGGCCCTCACCTCCCTTACATCGAACAGGAGTGCAGTCCGCC	3900	Dd	4921	ACCACGGGCCCCGTGACGCCCTTCCCGCGCCAAATTTATTAGGGCGCTGTGGCGGGTG	4980
Dd	3841	GATGAGATGGAGTGGCCCTCACCTCCCTTACATCGAACAGGAGTGCAGTCCGCC	3900	Qy	4981	GCTGTGAGGAGTACGTGAGGTTTACCGGGTGGGGATTTTCCACTACGTGACGCGCATG	5040
Qy	3901	GAACAATTCAAACAGAAAGCAATCGGGTGTCTGCAAAACAGCCCAAGCAAGCGAGGCT	3960	Dd	4981	GCTGTGAGGAGTACGTGAGGTTTACCGGGTGGGGATTTTCCACTACGTGACGCGCATG	5040
Dd	3901	GAACAATTCAAACAGAAAGCAATCGGGTGTCTGCAAAACAGCCCAAGCAAGCGAGGCT	3960	Qy	5041	ACCACCTGACAAAGTAAAGTCCCGGTGTAGGTTCCGGCCCCCGAAATTTCTTACAGAGTG	5100
Qy	3961	GCTGTCTCCGTGGTGAATCCAAAGTGGGAGCCCTCGAAGCCCTTCTGGCGGAAGCATATG	4020	Dd	5041	ACCACCTGACAAAGTAAAGTCCCGGTGTAGGTTCCGGCCCCCGAAATTTCTTACAGAGTG	5100
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Db 7441 TCATGGCTCAGGAAATCTGGGGTACCGCCCTTCGAGTCTGGAGACATCGGGCAGAACT 7500
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QY 7861 TTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
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Db 7921 TAGCTGTGAAGTCCCTGAGCCCTTGACTGCGAGAGTGTCTGATCTGGCCCTCTCTGC 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 14

ID ADP86271 standard; DNA; 11313 BP.
AC ADP86271;

XX 23-SEP-2004 (first entry)

XX Hepatitis C virus Con-1 replicon I377/NS3-3' derived plasmid DNA, p2S10.

XX Hepatitis C virus; HCV; anti-HCV agent; HCV infection; therapy; plasmid;

XX ds.

XX Hepatitis C virus.

XX WO200405216-A2.

XX 01-JUL-2004.

XX 12-DEC-2003; 2003WO-US039722.

XX 13-DEC-2002; 2002US-0433303P.

XX (FOX-) FOX CHASE CANCER CENT.
PA Zhu Q, Guo J, Seeger C;
PI WPI; 2004-488079/46.
XX New cell-line that replicates hepatitis C virus (HCV), where the cell
line is selected from a non-human cell line and a human non-hepatic cell
line, useful for identifying anti-HCV agents for treating HCV infections.
XX Example III; SEQ ID NO 8; 130pp; English.
XX The present invention provides hepatitis C virus (HCV) replication cells
and cell lines derived from human non-hepatic cells or non-human cells.
XX The invention is useful for identifying anti-HCV agents for treating HCV
infections. The present sequence is hepatitis C virus Con-1 replicon
CC I377/NS3-3' derived plasmid DNA.
XX Sequence 11313 BP; 2346 A; 3334 C; 3153 G; 2480 T; 0 U; 0 Other;

Query Match 100.0%; Score 7988.8; DB 12; Length 11313;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7990; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGCCCCGATTGGGGCGCACATCCACATAGATCACTCCCTGTGAGGAACACTCTG 60
Db 1 GCCAGCCCCGATTGGGGCGCACATCCACATAGATCACTCCCTGTGAGGAACACTCTG 60
QY 61 TCTTACGCGAAGAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120
Db 61 TCTTACGCGAAGAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120
QY 121 CCCCTCCGCGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATGGCAG 180
Db 121 CCCCTCCGCGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATGGCAG 180
QY 181 GAGCAGCGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGGCGTCCGCC 240
Db 181 GAGCAGCGGTCTCTTTCTTGGATCAACCCGCTCAATGCTGGAGATTGGGCGTCCGCC 240
QY 241 GCGAGATGCTAGCCGAGTAGTGTGGTCCGAAAGGCGCTTGTGTTACTGCTCTGATAGG 300
Db 241 GCGAGATGCTAGCCGAGTAGTGTGGTCCGAAAGGCGCTTGTGTTACTGCTCTGATAGG 300
QY 301 GTGCTTCGAGTGCCTCCGCGAGGTCTCTAGACCGTGCACCATGAGCAGCAATCCTAAAC 360
Db 301 GTGCTTCGAGTGCCTCCGCGAGGTCTCTAGACCGTGCACCATGAGCAGCAATCCTAAAC 360
QY 361 CTCAAGAGAAACCAAAGGCGCGCCATGATTGAACAGATGATGATGACGAGGTTCTC 420
Db 361 CTCAAGAGAAACCAAAGGCGCGCCATGATTGAACAGATGATGATGACGAGGTTCTC 420
QY 421 CGGCGCTTGGTGGAGAGGCTATTCGGCTATGCTGGGCAACAGACAACTCGCTGCT 480
Db 421 CGGCGCTTGGTGGAGAGGCTATTCGGCTATGCTGGGCAACAGACAACTCGCTGCT 480
QY 481 CTGATGCGCGCTGTTCGGCTGTGAGCGGCGCGCGGCTTCTTTTGTCAAGACCG 540
Db 481 CTGATGCGCGCTGTTCGGCTGTGAGCGGCGCGCGGCTTCTTTTGTCAAGACCG 540
QY 541 ACCTGTCCGGTGCCTGAAATGAACTGCAAGGAGGCGGCGGCTATCTGTTGGTGGCCA 600
Db 541 ACCTGTCCGGTGCCTGAAATGAACTGCAAGGAGGCGGCGGCTATCTGTTGGTGGCCA 600
QY 601 CGAGGGGCTTCTTGGCGAGCTGTGCTCGAGCTGTCTGAGCTGTCTGAGCGGAGGACTGCG 660
Db 601 CGAGGGGCTTCTTGGCGAGCTGTGCTCGAGCTGTCTGAGCTGTCTGAGCGGAGGACTGCG 660
QY 661 TGCTATTGGCGAAGTGCCTGGGCGAGGATCTCTGTCTATCTCACCTTCTCTCCGAGA 720
Db 661 TGCTATTGGCGAAGTGCCTGGGCGAGGATCTCTGTCTATCTCACCTTCTCTCCGAGA 720

QY	721	AAAGTATCCATCAATGCGCTGATGCAATTCGCGCGGCTGCATACGCTTGATCCGGCTACCTGCC	780
DB	721	AAAGTATCCATCAATGCGCTGATGCAATTCGCGCGGCTGCATACGCTTGATCCGGCTACCTGCC	780
QY	781	CAATTGACACCAACGGAACATCGCATTCGACGAGCAGTACTCGGATGGAAGCGGTC	840
DB	781	CAATTGACACCAACGGAACATCGCATTCGACGAGCAGTACTCGGATGGAAGCGGTC	840
QY	841	TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCACGCCCACTGTTTCG	900
DB	841	TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCACGCCCACTGTTTCG	900
QY	901	CCAGGCTCAAGCGCGCATGCGCGACGAGGATCTCGTGGTGAATCATGATCGATCGGATCGCT	960
DB	901	CCAGGCTCAAGCGCGCATGCGCGACGAGGATCTCGTGGTGAATCATGATCGGATCGGATCGCT	960
QY	961	GCTTCCCGAATATCATGTTGGAAATGCGCGTTCCTGGATTCATGATTCGATTCGATTCG	1020
DB	961	GCTTCCCGAATATCATGTTGGAAATGCGCGTTCCTGGATTCATGATTCGATTCGATTCG	1020
QY	1021	TGGGTGTGCGGACCGCTATCAGACATAGCGTTGGCTACCGCTGATATTCGTAAGAGC	1080
DB	1021	TGGGTGTGCGGACCGCTATCAGACATAGCGTTGGCTACCGCTGATATTCGTAAGAGC	1080
QY	1081	TTGGCGGGAATGGCTGACCGTTCCTGCTGCTTTACGGTATCCCGCTCCCGATTCGC	1140
DB	1081	TTGGCGGGAATGGCTGACCGTTCCTGCTGCTTTACGGTATCCCGCTCCCGATTCGC	1140
QY	1141	AGCGCATCGCTTCATCGCCTTCCTGACGAGTTCCTGCTGAGTTTAAACAGACCAACG	1200
DB	1141	AGCGCATCGCTTCATCGCCTTCCTGACGAGTTCCTGCTGAGTTTAAACAGACCAACG	1200
QY	1201	GTTTCCCTCTAGCGGATCAATTCCGCGCCTCTCCCTCCCGCCCTAACGTTACTGGC	1260
DB	1201	GTTTCCCTCTAGCGGATCAATTCCGCGCCTCTCCCTCCCGCCCTAACGTTACTGGC	1260
QY	1261	CGAAGCGCTTGGAAATAGGCGGTGTCGTTGTCTATATGTTATTTCCACCATATG	1320
DB	1261	CGAAGCGCTTGGAAATAGGCGGTGTCGTTGTCTATATGTTATTTCCACCATATG	1320
QY	1321	CCGTCCTTTGGCAATGAGGGCCGGAACCTGGCCCTGCTCTTTGACGAGATTCCT	1380
DB	1321	CCGTCCTTTGGCAATGAGGGCCGGAACCTGGCCCTGCTCTTTGACGAGATTCCT	1380
QY	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCGTTGATGTCGTAAGAGAGCA	1440
DB	1381	AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCGTTGATGTCGTAAGAGAGCA	1440
QY	1441	GTTCTCTGAAAGTCTCTGAGACAAACACGTCGTAGCGACCTTTGACGCGAGCG	1500
DB	1441	GTTCTCTGAAAGTCTCTGAGACAAACACGTCGTAGCGACCTTTGACGCGAGCG	1500
QY	1501	AACCCCGCCTGGCGACGTCCTCTGCGGCCAAAGGCCAGTGTATAGATACCT	1560
DB	1501	AACCCCGCCTGGCGACGTCCTCTGCGGCCAAAGGCCAGTGTATAGATACCT	1560
QY	1561	GCAAGCGGCAACACCCAGTCGAGTTGAGTTGATGTCGTAAGAGAGTCAAA	1620
DB	1561	GCAAGCGGCAACACCCAGTCGAGTTGAGTTGATGTCGTAAGAGAGTCAAA	1620
QY	1621	TGSGCTCTCAAGGATTTCAACAGGGGCTGAAGATGCCAGAGGTACCCATGCT	1680
DB	1621	TGSGCTCTCAAGGATTTCAACAGGGGCTGAAGATGCCAGAGGTACCCATGCT	1680
QY	1681	ATGGATCTCATCTGGGGCTCGGTGCATGCTTTACATGTTGTTAGTCGAGGTTAAA	1740
DB	1681	ATGGATCTCATCTGGGGCTCGGTGCATGCTTTACATGTTGTTAGTCGAGGTTAAA	1740
QY	1741	AACGCTTAGGCCCCCGAACCAGCGGACGTGTTTTCTTTGAAAAACACCATATACC	1800
DB	1741	AACGCTTAGGCCCCCGAACCAGCGGACGTGTTTTCTTTGAAAAACACCATATACC	1800
QY	1801	ATGGCGCTATTACGGCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCT	1860

1801	ATGCGGCTATTACGGCCTACTCCCAACAGACGCGAGGCCCTACTTGGCTGCATCACTACT	1860
1861	AGCTCACAGCGCGGACAGGACAGGACAGGTCGAGGGGGAGGTCAAAGTGTCTCCACCGCA	1920
1861	AGCTCACAGCGCGGACAGGAACAGGTCGAGGGGGAGGTCAAAGTGTCTCCACCGCA	1920
1921	ACAAATCTTTCTGTGCGACTCGCTCAATGGCGTGTGTGGACTCTCTATCATGTGCG	1980
1921	ACAAATCTTTCTGTGCGACTCGCTCAATGGCGTGTGTGGACTCTCTATCATGTGCG	1980
1981	GGCTCAAGACCTTGTGCGGCCCAAGAGGCCCATAACCCAAATGTACCAATGTGGAC	2040
1981	GGCTCAAGACCTTGTGCGGCCCAAGAGGCCCATAACCCAAATGTACCAATGTGGAC	2040
2041	CAGGACTCGTGGCTGGCAAGCGCCCCGGGGCGGTCCTTGCACATGCACCTGC	2100
2041	CAGGACTCGTGGCAAGCGCCCCGGGGCGGTCCTTGCACATGCACCTGC	2100
2101	GGCAGCTCGGACCTTTACTTGTGTCAGAGGCATGCCGATGTCATTCCCGTGC	2160
2101	GGCAGCTCGGACCTTTACTTGTGTCAGAGGCATGCCGATGTCATTCCCGTGC	2160
2161	GGCGACAGAGGGGAGCCTACTCTCCCAAGCGCGTCTCCTACTTGAAGGGCTCTTCG	2220
2161	GGCGACAGAGGGGAGCCTACTCTCCCAAGCGCGTCTCCTACTTGAAGGGCTCTTCG	2220
2221	GGCGGTCACACTGCTCTGCCCCCTCGGGGACGCTGTGGGCATCTTTTGGGCTCGCTGTGC	2280
2221	GGCGGTCACACTGCTCTGCCCCCTCGGGGACGCTGTGGGCATCTTTTGGGCTCGCTGTGC	2280
2281	ACCGAGGGGTTGCGAAGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG	2340
2281	ACCGAGGGGTTGCGAAGCGGTGGACTTTGTACCCGTCGAGTCTATGGAACCACTATG	2340
2341	CGGTCCCGGCTTTTCAGGACAACTCGTCCCTCCGGCGGTACCGCAGACATTC	2400
2341	CGGTCCCGGCTTTTCAGGACAACTCGTCCCTCCGGCGGTACCGCAGACATTC	2400
2401	GCCCATCTACAGCCCTACTGGTAGCGCAGAGCACTAAGGTGCGGGCTCGGTATGGA	2460
2401	GCCCATCTACAGCCCTACTGGTAGCGCAGAGCACTAAGGTGCGGGCTCGGTATGGA	2460
2461	GCCCAAGGTTAAGGTGCTTGTCTGAACCGTCCGTCGCGCCACCCCTAGGTTTCGGG	2520
2461	GCCCAAGGTTAAGGTGCTTGTCTGAACCGTCCGTCGCGCCACCCCTAGGTTTCGGG	2520
2521	GGGTATGTCTAAGGCAATGGTATCGACCTTAACATCAGAACCGGGGTAAAGACCATC	2580
2521	GGGTATGTCTAAGGCAATGGTATCGACCTTAACATCAGAACCGGGGTAAAGACCATC	2580
2581	ACCAAGGTTGCCCATCAGTCTCAGCTTACCGTATGGCAAGTTTCTTGGCGACGGTGTGC	2640
2581	ACCAAGGTTGCCCATCAGTCTCAGCTTACCGTATGGCAAGTTTCTTGGCGACGGTGTGC	2640
2641	TCTGGGGCGCTATGACATCAATATGTGATGAGTGCCACTCACTGACTCGACCACT	2700
2641	TCTGGGGCGCTATGACATCAATATGTGATGAGTGCCACTCACTGACTCGACCACT	2700
2701	ATCTGGGCATGGGACAGTCTCGGACCAAGCGGACGGTGGAGCGGACTCGTGGTG	2760
2701	ATCTGGGCATGGGACAGTCTCGGACCAAGCGGACGGTGGAGCGGACTCGTGGTG	2760
2761	CTCGCCACCGCTACGCTTCGGGATCGGTACCGTGGCCATCCAAACATCGAGGAGGTG	2820
2761	CTCGCCACCGCTACGCTTCGGGATCGGTACCGTGGCCATCCAAACATCGAGGAGGTG	2820
2821	GCTCTGTCCAGCACTGGAGAAATCCCCTTTTATGGCAAGCCATCCCCATCGAGACCATC	2880
2821	GCTCTGTCCAGCACTGGAGAAATCCCCTTTTATGGCAAGCCATCCCCATCGAGACCATC	2880
2881	AAGGGGGGAGGCACTTCAATTTCTGCCATCTCCAAAGAAATGTGATGAGCTCGCGCG	2940

Db 2881 AAGGGGGGAGCACCCTCATTTTCTGCGCATTCACAGAGAAATGTGATGAGCTCGCCGG 2940
Qy 2941 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTTACCGGGGCTTGTATGTATCCGTC 3000
Db 2941 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTTACCGGGGCTTGTATGTATCCGTC 3000
Qy 3001 ATACCACTAGCGGAGACGTCTATTGTGTAGCAACGAGCGCTCTAATGACGGCTTTTACC 3060
Db 3001 ATACCACTAGCGGAGACGTCTATTGTGTAGCAACGAGCGCTCTAATGACGGCTTTTACC 3060
Qy 3061 GCGATTTCCGACTCAGTGTACGACTGCAATACATGTGTCAACGAGACAGTTCGACTTCAG 3120
Db 3061 GCGATTTCCGACTCAGTGTACGACTGCAATACATGTGTCAACGAGACAGTTCGACTTCAG 3120
Qy 3121 CTGGACCCGACCTTACCAATGAGACGACGACGCTGCCACAGACGCGGTGTACGCTCG 3180
Db 3121 CTGGACCCGACCTTACCAATGAGACGACGACGCTGCCACAGACGCGGTGTACGCTCG 3180
Qy 3181 CAGCGGAGGAGGAGTGTGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGAGGAGGAGTGTGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240
Qy 3241 GAACGGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGTGT 3300
Db 3241 GAACGGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGTGT 3300
Qy 3301 GCTTGTACGAGTACGCGCCGCGGAGACCTCAGTTAGTTGGGCTTACCTAAACACA 3360
Db 3301 GCTTGTGTACGAGTACGCGCCGCGGAGACCTCAGTTAGTTGGGCTTACCTAAACACA 3360
Qy 3361 CAGGGTTGCGCTCTGCCAGGACCATCTCGAGTTCTGGGAGAGCGTCTTTACAGGCGTC 3420
Db 3361 CAGGGTTGCGCTCTGCCAGGACCATCTCGAGTTCTGGGAGAGCGTCTTTACAGGCGTC 3420
Qy 3421 ACCACATAGACGCCCATTTCTTGTCCGACCTAAGCAGGACGAGACAACTTCCCTTAC 3480
Db 3421 ACCACATAGACGCCCATTTCTTGTCCGACCTAAGCAGGACGAGACAACTTCCCTTAC 3480
Qy 3481 CTGTTAGCATACAGGCTACGTTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Db 3481 CTGTTAGCATACAGGCTACGTTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Qy 3541 CAAATGTGGAGTGTCTCATACGCTAAAGCTACGCTGACAGGGCCAAAGCCCTCTGCTG 3600
Db 3541 CAAATGTGGAGTGTCTCATACGCTAAAGCTACGCTGACAGGGCCAAAGCCCTCTGCTG 3600
Qy 3601 TATAGGCTGGAGCCGTTCAAAACGAGGTTACTACCAACACCCCAATACCAATATATC 3660
Db 3601 TATAGGCTGGAGCCGTTCAAAACGAGGTTACTACCAACACCCCAATACCAATATATC 3660
Qy 3661 ATGGCATGCATGTCGGCTGACCTGAGGTGCTCAGGACACCTGGGTCTGTTAGGCGGA 3720
Db 3661 ATGGCATGCATGTCGGCTGACCTGAGGTGCTCAGGACACCTGGGTCTGTTAGGCGGA 3720
Qy 3721 GTCTAGCAGTCTGCGCGCTATTGCTGACAAACAGGACGCTGGTCAITTTGGGCGAG 3780
Db 3721 GTCTAGCAGTCTGCGCGCTATTGCTGACAAACAGGACGCTGGTCAITTTGGGCGAG 3780
Qy 3781 ATCATCTTGTCCGAAAGCCGCGCATCATTCCTCCGACAGGAGTCTTTACGGGAGTTC 3840
Db 3781 ATCATCTTGTCCGAAAGCCGCGCATCATTCCTCCGACAGGAGTCTTTACGGGAGTTC 3840
Qy 3841 GATGAGATGAGAGTGGCGCTCACACCTCCCTTACATCGAACAGGAAATGACGCTCGCC 3900
Db 3841 GATGAGATGAGAGTGGCGCTCACACCTCCCTTACATCGAACAGGAAATGACGCTCGCC 3900
Qy 3901 GAACAATTCAACAGAGAGCAATCGGTTGCTGCAAAACAGGCCCAACAGCGAGGCT 3960
Db 3901 GAACAATTCAACAGAGAGCAATCGGTTGCTGCAAAACAGGCCCAACAGCGAGGCT 3960
Qy 3961 GCTGCTCCGCTGGTGAATCCAAAGTGGGAGCCCTCGAAGCCCTCTGGGCGAGCATATG 4020
Db 3961 GCTGCTCCGCTGGTGAATCCAAAGTGGGAGCCCTCGAAGCCCTCTGGGCGAGCATATG 4020

Qy 4021 TGGAAATTTTCATCAGCGGGATACAAATATTATTAGCAGGCTTGTTCACCTGTGCTTGGGAACCC 4080
Db 4021 TGGAAATTTTCATCAGCGGGATACAAATATTATTAGCAGGCTTGTTCACCTGTGCTTGGGAACCC 4080
Qy 4081 GCGATAGCATCTACTGATGGCAITTCACAGCTCTATCACCAGCCGCTACACCAACAAAT 4140
Db 4081 GCGATAGCATCTACTGATGGCAITTCACAGCTCTATCACCAGCCGCTACACCAACAAAT 4140
Qy 4141 ACCCTCCTGTTTAAACATCTCGGGGATGGGTGGCGCCCAACTTGTCTCTCCACGCGCT 4200
Db 4141 ACCCTCCTGTTTAAACATCTCGGGGATGGGTGGCGCCCAACTTGTCTCTCCACGCGCT 4200
Qy 4201 GCTTCTGCTTTTCGTAGGCGCCGCGCATCTGCTGAGCGGCTTGTGGCAGCATAGGCGCTTGG 4260
Db 4201 GCTTCTGCTTTTCGTAGGCGCCGCGCATCTGCTGAGCGGCTTGTGGCAGCATAGGCGCTTGG 4260
Qy 4261 AAGTGTCTTGTGGATATTTGGCAGGTTATGGAGCGGGTGGCAGCGGCTCTGTGGCC 4320
Db 4261 AAGTGTCTTGTGGATATTTGGCAGGTTATGGAGCGGGTGGCAGCGGCTCTGTGGCC 4320
Qy 4321 TTTAAGGTTCATGACGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTTACTCCCTGCT 4380
Db 4321 TTTAAGGTTCATGACGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTTACTCCCTGCT 4380
Qy 4381 ATCTCTCTCCCTGGCGCCCTTAGTCTGCGGGTCTGTGCGCAGGATACTGCGTCCGTCAC 4440
Db 4381 ATCTCTCTCCCTGGCGCCCTTAGTCTGCGGGTCTGTGCGCAGGATACTGCGTCCGTCAC 4440
Qy 4441 GTGGGCCAGGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTTCGCTTCCGCG 4500
Db 4441 GTGGGCCAGGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTTCGCTTCCGCG 4500
Qy 4501 GGTAAACACGCTCTCCCGCCACGCACTATGTCCCTGAGAGCGACGCTGCAGACGCTGCT 4560
Db 4501 GGTAAACACGCTCTCCCGCCACGCACTATGTCCCTGAGAGCGACGCTGCAGACGCTGCT 4560
Qy 4561 CAGATCTCTCTAGTCTTACCATCATCTCAGCTGCTGAAGAGGCTTACCAGTGGATCAAC 4620
Db 4561 CAGATCTCTCTAGTCTTACCATCATCTCAGCTGCTGAAGAGGCTTACCAGTGGATCAAC 4620
Qy 4621 GAGGACTGTCTCCAGCCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATGGATATGC 4680
Db 4621 GAGGACTGTCTCCAGCCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATGGATATGC 4680
Qy 4681 ACSTGTGTGATCTGATTTCAAGACCTGCTCCAGTCCAGCTCCCTGCGCGGATTCGCGGA 4740
Db 4681 ACSTGTGTGATCTGATTTCAAGACCTGCTCCAGTCCAGCTCCCTGCGCGGATTCGCGGA 4740
Qy 4741 GTCCCTTCTTCTCATGTCACAGTGGGTACAGGGAGTCTGCGGGGGGACGCGCATATG 4800
Db 4741 GTCCCTTCTTCTCATGTCACAGTGGGTACAGGGAGTCTGCGGGGGGACGCGCATATG 4800
Qy 4801 CAAACCACTGCCCATGTGGAGCAGATCACCGGACATGTGAAAAACGGTTCCATGAGG 4860
Db 4801 CAAACCACTGCCCATGTGGAGCAGATCACCGGACATGTGAAAAACGGTTCCATGAGG 4860
Qy 4861 ATCTGCGGCGCTTAGGACCTGTAGTAAACACGTTGGCATGGAAATTCCTCCCATTAACGCGTAC 4920
Db 4861 ATCTGCGGCGCTTAGGACCTGTAGTAAACACGTTGGCATGGAAATTCCTCCCATTAACGCGTAC 4920
Qy 4921 ACCAGGGCCCTTGGAACCGCTCCCGCGGCGCAATTTATTCTAGGGCGCTGTGGCGGCTG 4980
Db 4921 ACCAGGGCCCTTGGAACCGCTCCCGCGGCGCAATTTATTCTAGGGCGCTGTGGCGGCTG 4980
Qy 4981 GCTGCTGAGGAGTACGTTGAGGATGTTACGCGGTGGGGATTTCCACTACGTACGCGGCGATG 5040
Db 4981 GCTGCTGAGGAGTACGTTGAGGATGTTACGCGGTGGGGATTTCCACTACGTACGCGGCGATG 5040
Qy 5041 ACCACTGACAAAGTAAAGTCCCGGTGTAGGTTCCGGCCCCCGAATTTCTTTCAGAAAGTG 5100
Db 5041 ACCACTGACAAAGTAAAGTCCCGGTGTAGGTTCCGGCCCCCGAATTTCTTTCAGAAAGTG 5100

QY 5101 GATGGGTGGGTGACAGGTACGCTCCAGCGTGCAAAACCCCTCCTACGGGAGGAGTC 5160
DB |||||
QY 5101 GATGGGTGGGTGACAGGTACGCTCCAGCGTGCAAAACCCCTCCTACGGGAGGAGTC 5160
DB |||||
QY 5161 ACATTCCTGGTGGGTCAATCAATACCTGGTGGGTACAGTCCCATCGAGCCCGAA 5220
DB |||||
QY 5161 ACATTCCTGGTGGGTCAATCAATACCTGGTGGGTACAGTCCCATCGAGCCCGAA 5220
DB |||||
QY 5221 CCGGAGTAGAGTGCTCACTTCCATGCTACCGACCCCTCCCAATACCGCGGAGACG 5280
DB |||||
QY 5221 CCGGAGTAGAGTGCTCACTTCCATGCTACCGACCCCTCCCAATACCGCGGAGACG 5280
DB |||||
QY 5281 GCTAAGCTGAGCTGGCAGGGGATCTCCCTCTCTGGCAGGTCACTACGCTACGCTACG 5340
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QY 5281 GCTAAGCTGAGCTGGCAGGGGATCTCCCTCTCTGGCAGGTCACTACGCTACGCTACG 5340
DB |||||
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DB |||||
QY 5401 CTATCGAGGCAACCTCTCTGGCGGAGAGATGGCGGGAACATCAACCGCGTGAG 5460
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QY 5461 TCAGAAATAGGTAGTAATTTGCACTCTTTCGAGCCGCTCCAGCGGAGAGATGAG 5520
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DB |||||
QY 5521 AGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCCAGAAATTCCTTCGAGCGATG 5580
DB |||||
QY 5581 CCCATATGGGACCGCCGGATTACAACTCTTTCGAGGTCCAGAAATTCCTTCGAGCGATG 5580
DB |||||
QY 5581 CCCATATGGGACCGCCGGATTACAACTCTTTCGAGGTCCAGAAATTCCTTCGAGCGATG 5580
DB |||||
QY 5641 TACGTCCCTCCAGTGGTACAGGGTGTCATTCGCGCTCCAGGCTCCGATACCA 5700
DB |||||
QY 5641 TACGTCCCTCCAGTGGTACAGGGTGTCATTCGCGCTCCAGGCTCCGATACCA 5700
DB |||||
QY 5701 CCTCCAGGAGAGAGACGTTGTCTGTGCAAACTACCGGTCTCTTCGCTTCGCG 5760
DB |||||
QY 5701 CCTCCAGGAGAGAGACGTTGTCTGTGCAAACTACCGGTCTCTTCGCTTCGCG 5760
DB |||||
QY 5761 GAGTCCGCAAAAGACCTTCGGCAGTCCGAAFCGTCGCGCTCGACAGCGGACCGCA 5820
DB |||||
QY 5761 GAGTCCGCAAAAGACCTTCGGCAGTCCGAAFCGTCGCGCTCGACAGCGGACCGCA 5820
DB |||||
QY 5821 ACGGCTCTCTGACAGCCCTCCGACGCGGACCGGAGTCCGATCTCAGCGAGGCTCTG 5880
DB |||||
QY 5821 ACGGCTCTCTGACAGCCCTCCGACGCGGACCGGAGTCCGATCTCAGCGAGGCTCTG 5880
DB |||||
QY 5881 TCCTCATGCCCCCTTGAGGGGAGCCGGGGATCCCGATCTCAGCGAGGCTCTG 5940
DB |||||
QY 5881 TCCTCATGCCCCCTTGAGGGGAGCCGGGGATCCCGATCTCAGCGAGGCTCTG 5940
DB |||||
QY 5941 TCTACCGTAGCGAGGCTAGTAGGACGTCGTCTGCTGCTCGATCTCAGCTCAGATGG 6000
DB |||||
QY 5941 TCTACCGTAGCGAGGCTAGTAGGACGTCGTCTGCTGCTCGATCTCAGCTCAGATGG 6000
DB |||||
QY 6001 ACAGGCGCTGATACGCGCATCGCTGGGAGAAACCAAGCTGCCATCAATGCACTG 6060
DB |||||
QY 6001 ACAGGCGCTGATACGCGCATCGCTGGGAGAAACCAAGCTGCCATCAATGCACTG 6060
DB |||||
QY 6061 AGCAACTCTTGTCCGTACCAACAATCTGCTATGCTACAACTCTCGACGCAAGC 6120
DB |||||
QY 6061 AGCAACTCTTGTCCGTACCAACAATCTGCTATGCTACAACTCTCGACGCAAGC 6120
DB |||||
QY 6121 CTGCGCAGAGAGGTCACTTTGACAGTCTCAGGTCTCGAGTCTCGAGTCTCGAGTCTG 6180
DB |||||
QY 6121 CTGCGCAGAGAGGTCACTTTGACAGTCTCAGGTCTCGAGTCTCGAGTCTCGAGTCTG 6180
DB |||||
QY 6181 GTGCTCAAGGAGATGAAGCGAGGCGTCCACAGTTAAGGCTTAACTTCTATCCGTGGAG 6240
DB |||||

DB |||||
QY 6181 GTGCTCAAGSAGATGAGCGAAGGCGTCCACAGTTAAGCTAAACTTCTATCCGTGGAG 6240
DB |||||
QY 6241 GAAGCTGTAGCTGACGCCCCCACCATTGCGCCAGATCTAAATTTGGCTATGGGCAAG 6300
DB |||||
QY 6241 GAAGCTGTAGCTGACGCCCCCACCATTGCGCCAGATCTAAATTTGGCTATGGGCAAG 6300
DB |||||
QY 6301 GAGCTCCGGAACCTATCCAGCAAGCGGTTAAACCATCCGCTCCGTGTGGAAGACTTG 6360
DB |||||
QY 6301 GAGCTCCGGAACCTATCCAGCAAGCGGTTAAACCATCCGCTCCGTGTGGAAGACTTG 6360
DB |||||
QY 6361 CTGGAAGACACTGACACCAATTCACACCACTCATGCGCAAAATAGAGTTTCTGC 6420
DB |||||
QY 6361 CTGGAAGACACTGACACCAATTCACACCACTCATGCGCAAAATAGAGTTTCTGC 6420
DB |||||
QY 6421 GTCCAAACAGAGAGGGGGCGCAAGCCAGCTCGCTTATCGTATTCACAGATTGGG 6480
DB |||||
QY 6421 GTCCAAACAGAGAGGGGGCGCAAGCCAGCTCGCTTATCGTATTCACAGATTGGG 6480
DB |||||
QY 6481 GTTCGTGTGGGAGAAATGGCCCTTTACGATGTGCTTCCACCTCCCTCAGGCCGTG 6540
DB |||||
QY 6481 GTTCGTGTGGGAGAAATGGCCCTTTACGATGTGCTTCCACCTCCCTCAGGCCGTG 6540
DB |||||
QY 6541 ATGGCTCTTCATACGGAATTCCAATACTCTCTCGACAGCGGTCGAGTCTCTGTGAAT 6600
DB |||||
QY 6541 ATGGCTCTTCATACGGAATTCCAATACTCTCTCGACAGCGGTCGAGTCTCTGTGAAT 6600
DB |||||
QY 6601 GCCTGGAAGCGAAGAAATGCCCTATGGCTTCGCAATATGACACCGCTGTTTGACTCA 6660
DB |||||
QY 6661 ACGETCACTGAGATGACATCCGTTGTGAGAGTCAATCTACCAATGTGTGACTTGCC 6720
DB |||||
QY 6661 ACGETCACTGAGATGACATCCGTTGTGAGAGTCAATCTACCAATGTGTGACTTGCC 6720
DB |||||
QY 6721 CCCGAAGCCAGACAGGCGCAATAGGTCGCTCACAGCGGCTTTACATCGGGGGCCCCCTG 6780
DB |||||
QY 6721 CCCGAAGCCAGACAGGCGCAATAGGTCGCTCACAGCGGCTTTACATCGGGGGCCCCCTG 6780
DB |||||
QY 6781 ACTAATTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGGCTGTAAGCTGTAAGC 6840
DB |||||
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QY 6841 ACCAGCTGCGGTAAATACCTTCATGTTACTTGAAGCCGCTGCGGCTGTAAGCTGCG 6900
DB |||||
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DB |||||
QY 6901 AAGTCTCAGGACTGCAAGTCTCGTATGCGGAGACGACCTTGTGCTTATCTGTGAAGC 6960
DB |||||
QY 6901 AAGTCTCAGGACTGCAAGTCTCGTATGCGGAGACGACCTTGTGCTTATCTGTGAAGC 6960
DB |||||
QY 6961 GCGGGAACCAAGAGGACGAGGCGCTACGGGCTTTCAGCGAGGCTATGACTAGATAC 7020
DB |||||
QY 6961 GCGGGAACCAAGAGGACGAGGCGCTACGGGCTTTCAGCGAGGCTATGACTAGATAC 7020
DB |||||
QY 7021 TCTGCCCCCTCGGAGCCCGCAACAGATAGCATGCTGAGTGTATACATATGC 7080
DB |||||
QY 7021 TCTGCCCCCTCGGAGCCCGCAACAGATAGCATGCTGAGTGTATACATATGC 7080
DB |||||
QY 7081 TCTTCAATGTGTGCTGCTGCGGAGACGACCTTGTGCAAAAGGCTGACTATCTCACCCGT 7140
DB |||||
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DB |||||
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DB |||||
QY 7141 GACCCCAACCCCTTTCGCGGGCTGCTGCGGAGACGACTAGACACACTCCAGTCAAT 7200
DB |||||
QY 7201 TCTGCTAGGCAACATCATGATGATGCGCCACCTTGTGCGCAAGGATGATCCTGATG 7260
DB |||||
QY 7201 TCTGCTAGGCAACATCATGATGATGCGCCACCTTGTGCGCAAGGATGATCCTGATG 7260
DB |||||
QY 7261 ACTCAATTTCTTCCATCTCTAGCTCAGGAGCACTTGAAGGCTTAACTTCTATCCGTGGAG 7320
DB |||||

Db	7261	ACTCATTTCTTCTCCTCATCTTCTAGCTCAGGACAACTTGAAAGACCTAGATTGTTCAG	7320
Qy	7321	ATCTACGGGGCGCTGTACTTCCATTGAGCCACTTGACCTCAGATCAATCAACGACTC	7380
Db	7321	ATCTACGGGGCGCTGTACTTCCATTGAGCCACTTGACCTCAGATCAATCAACGACTC	7380
Qy	7381	CATGGCCTTAGCGCATTTTCACTCCATAGTACTCTCCAGGTGAGATCAATAGGTGGCT	7440
Db	7381	CATGGCCTTAGCGCATTTTCACTCCATAGTACTCTCCAGGTGAGATCAATAGGTGGCT	7440
Qy	7441	TCATGGCTCAGAACTTGGGTGACCGCCTTGCAGTCTGGAGACATCGGCGCAGAACT	7500
Db	7441	TCATGGCTCAGAACTTGGGTGACCGCCTTGCAGTCTGGAGACATCGGCGCAGAACT	7500
Qy	7501	GTCCGGCTTAGGCTACTGTCCAGGGGGAGGGCTGCCACTTGTGGGAGTACCTTCTTC	7560
Db	7501	GTCCGGCTTAGGCTACTGTCCAGGGGGAGGGCTGCCACTTGTGGGAGTACCTTCTTC	7560
Qy	7561	AATGGGCGAGTAGGACCAAGCTCAAACTCACTCCCAATCCGGCTCGTCCCAAGTTGGAT	7620
Db	7561	AATGGGCGAGTAGGACCAAGCTCAAACTCACTCCCAATCCGGCTCGTCCCAAGTTGGAT	7620
Qy	7621	TTATCCAGCTGGTTCGTCTGTCTTACAGCGGGGAGACATATACAGCCTGTCTCGT	7680
Db	7621	TTATCCAGCTGGTTCGTCTGTCTTACAGCGGGGAGACATATACAGCCTGTCTCGT	7680
Qy	7681	GCCCGACCCCGCTGGTTCATGTGGTGGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT	7740
Db	7681	GCCCGACCCCGCTGGTTCATGTGGTGGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT	7740
Qy	7741	CTACTCCCAACCGATGACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	7800
Db	7741	CTACTCCCAACCGATGACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	7800
Qy	7801	TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	7801	TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Qy	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Qy	7921	TAGCTGTGAAGTCCCGTACCGCTTACCTGACGAGAGTCTGATCTGACCTCTCTGC	7980
Db	7921	TAGCTGTGAAGTCCCGTACCGCTTACCTGACGAGAGTCTGATCTGACCTCTCTGC	7980
Qy	7981	AGATCAAGTACT 7992	
Db	7981	AGATCAAGTACT 7992	
RESULT 15			
ID	AAD25322	standard; cDNA; 7989 BP.	
XX	AC	AAD25322;	
XX	DT	12-MAR-2002 (first entry)	
XX	DE	Hepatitis C virus (HCV) replbBartMan/Avall cDNA.	
XX	KW	Hepatitis C virus; HCV; transfection; infection; virus neutralisation;	
KW	ss.	gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;	
XX	OS	Hepatitis C virus.	
XX	Key	Location/Qualifiers	
FT	CDS	1801..7758	
FT	FT	/tag= a	
FT	FT	/product= "HCVreplbBartMan polyprotein"	
FT	FT	7766	
FT	FT	misc_feature	
FT	FT	/tag= b	

/note= "Nucleotide creating Availi site"

WO200189364-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-US016822.

23-MAY-2000; 2000US-00576989.

(UNIW) UNIV WASHINGTON.

Rice CM, Blight KJ;

WPI: 2002-066755/09.

P-PSDB; AEL1517.

Hepatitis C virus variants having greater transfection efficiency and ability to survive subpassage, useful as a vaccine for immunizing primate to the virus, comprise non-naturally occurring viral sequences.

Claim 44; Page 69-71; 174pp; English.

The invention relates to Hepatitis C virus (HCV) variants which include polynucleotides comprising non-naturally occurring HCV sequence and HCV variants that have a transfection efficiency and ability to survive subpassage greater than HCV that have wild-type polypeptide coding regions. The polynucleotides of the invention are useful for identifying a cell line that is permissive for infection with HCV and detecting replication of HCV in cells of the cell line. They are also useful for testing a compound for anti-viral properties and for inhibiting HCV infection. They are also useful for in vivo assays for virus neutralisation, attachment, penetration and entry, structure/function studies on HCV proteins and RNA elements and identification of new antiviral targets, a systematic survey of cell culture systems and conditions to identify those that support wild-type and variant HCV RNA replication and particle release, production of adaptive HCV variants capable of more efficiency tissue or species tropism, establishment of alternative animal models for inhibitor evaluation including those supporting HCV variant replication, development of cell-free HCV replication assays, production of immunogenic HCV particles for vaccination, engineering of attenuated or derivative HCV derivatives for expression of heterologous gene products for gene therapy and vaccine applications and for utilisation of the HCV glycoproteins for targeted delivery of therapeutic agents to the liver or other cell types with appropriate receptors. Vaccine comprising these sequences is useful for inducing immunoprotection to HCV in a primate. The present sequence is Hepatitis C virus (HCV) replbBartMan/Avall cDNA

Sequence 7989 BP; 1647 A; 2369 C; 2242 G; 1731 T; 0 U; 0 Other;

Query Match 99.9%; Score 7987.4; DB 6; Length 7989;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7988; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60

Db 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTG 60

Qy 61 TCTTCCAGCAAGACGCTGTAGCCATGGCTTAGTATGAGTCTCGTCAGCTCCAGGAC 120

Db 61 TCTTCCAGCAAGACGCTGTAGCCATGGCTTAGTATGAGTCTCGTCAGCTCCAGGAC 120

Qy 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180

Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180

Qy 181 GACGACCGGGTCTCTTTCTTGGATCAACCGCTCAATGCTCGAGATTGGGGTGCCCC 240

Db 181 GACGACCGGGTCTCTTTCTTGGATCAACCGCTCAATGCTCGAGATTGGGGTGCCCC 240

QY 241 GCAGAGCTGCTAGCCGAGTAGTGTGGTCCGCGAAAGCCCTTGTGTAAGG 300
Db 241 GCAGAGCTGCTAGCCGAGTAGTGTGGTCCGCGAAAGCCCTTGTGTAAGG 300
QY 301 GTGCTTCGAGTGCCTCCGCGAGTCTCGTAGACCGTGCACATGACGACGAATCCTAAAC 360
Db 301 GTGCTTCGAGTGCCTCCGCGAGTCTCGTAGACCGTGCACATGAGCAGCAATCCTAAAC 360
QY 361 CTCAGAGAAACCAAGGCGCGCCATGATTGAACAAGATGGATTGCACGCGAGTTCTC 420
Db 361 CTCAGAGAAACCAAGGCGCGCCATGATTGAACAAGATGGATTGCACGCGAGTTCTC 420
QY 421 CGCGCGCTTCGCTGGAGAGCTATTCCGCTATGACTGGGACACACAGCAATCGGCTGCT 480
Db 421 CGCGCGCTTCGCTGGAGAGCTATTCCGCTATGACTGGGACACACAGCAATCGGCTGCT 480
QY 481 CTGATGCGCGCTGTTCCGCGCTGTACAGCGAGGGCGCGCGTCTTTTGTCAAGACCG 540
Db 481 CTGATGCGCGCTGTTCCGCGCTGTACAGCGAGGGCGCGCGTCTTTTGTCAAGACCG 540
QY 541 ACTGTGCGGTGCCCTGAATGAATCTGAGGACGAGGACGCGCGCTATCGTGGCTGGCCA 600
Db 541 ACTGTGCGGTGCCCTGAATGAATCTGAGGACGAGGACGCGCGCTATCGTGGCTGGCCA 600
QY 601 CGACGGCGCTTCCTTCGCGAGCTGTGCTCGAGTGTCTGCTGAAGCGGGAAGGACTGGC 660
Db 601 CGACGGCGCTTCCTTCGCGAGCTGTGCTCGAGTGTCTGCTGAAGCGGGAAGGACTGGC 660
QY 661 TGTATTGGGCGAAGTGCCTGGGCGAGGATCTCTGTGATCTACCTGTGCTTCCTGCGGAGA 720
Db 661 TGTATTGGGCGAAGTGCCTGGGCGAGGATCTCTGTGATCTACCTGTGCTTCCTGCGGAGA 720
QY 721 AAGTATCCATGCTGCTGATGCAATGCGCGCTGCTGATACGCTGATCCGCTACTCGCC 780
Db 721 AAGTATCCATGCTGCTGATGCAATGCGCGCTGCTGATACGCTGATCCGCTACTCGCC 780
QY 781 CATTCGACCAACAGGAAATCCGATCGACGAGACGTAAGTGGAGCGGTC 840
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QY 841 TTGTGATCAGGATGATCTGACGAGAGCATCAGGGCTCGCGCCAGCGGATCTGCTG 900
Db 841 TTGTGATCAGGATGATCTGACGAGAGCATCAGGGCTCGCGCCAGCGGATCTGCTG 900
QY 901 CAGGCTCAAGCGGCGATGCGCGAGGATCTCGTGTGACCCATGCGGATGCT 960
Db 901 CAGGCTCAAGCGGCGATGCGCGAGGATCTCGTGTGACCCATGCGGATGCT 960
QY 961 GCTTCCGGAATATCATGTTGGAATGCGCGCTTTCTGGATTATCGACTGTGGCGGC 1020
Db 961 GCTTCCGGAATATCATGTTGGAATGCGCGCTTTCTGGATTATCGACTGTGGCGGC 1020
QY 1021 TGGTGTGGCGGACCGCTATCAGACATAGCGTTGGCTACCGCTGATATCTGAGAGC 1080
Db 1021 TGGTGTGGCGGACCGCTATCAGACATAGCGTTGGCTACCGCTGATATCTGAGAGC 1080
QY 1081 TTGGCGGGAATGGCTGACCGCTTCCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
Db 1081 TTGGCGGGAATGGCTGACCGCTTCCTGCTTTACGGTATCGCGCTCCCGATTGCG 1140
QY 1141 AGCGCATCGCTTCATCGCTTCCTGACGAGTTCCTGAGTTTAAACAGACCAACG 1200
Db 1141 AGCGCATCGCTTCATCGCTTCCTGACGAGTTCCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTTACGTTACTGGC 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCTTACGTTACTGGC 1260
QY 1261 CGAAGCGCTTGGAAAGGCGGCTGTGCTGCTATATGTTATTTTCCACCAATG 1320
Db 1261 CGAAGCGCTTGGAAAGGCGGCTGTGCTGCTATATGTTATTTTCCACCAATG 1320
QY 1321 CCGTCTTTGGCAATGTGAGGGCCCGAAACCTGGCCCTGTCTTGTGACGAGATTCTCT 1380

Db 1321 CCGTCTTTTGGCAATGTGAGGGCCCGAAACCTGGCCCTGTCTTCTTGACGAGATTCTCT 1380
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Db 1381 AGGGGTCTTTCCCTCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGTCGTCAAGGAGCA 1440
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QY 1501 AACCCCCCACTCGCGACAGTGCCTCTCGCGCCAAAGCAAGCCAGTGTATGAAGATACACCT 1560
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Db 1621 TGGCTCTCTCAAGCGTATTCAAAGGGCTGAAGGATGCCAGAGGTACCCCATTTGT 1680
QY 1681 ATGGGATCTGATCTGGGCTCGGTGCACATGCTTTACATGTTTGTAGTCGAGGTTAAA 1740
Db 1681 ATGGGATCTGATCTGGGCTCGGTGCACATGCTTTACATGTTTGTAGTCGAGGTTAAA 1740
QY 1741 AACGCTTAGGCCCCCGGAACACGCGGACGTGTTTCTTTTGAAGAAACACCATATACC 1800
Db 1741 AACGCTTAGGCCCCCGGAACACGCGGACGTGTTTCTTTTGAAGAAACACCATATACC 1800
QY 1801 ATGGCGCTTTTACGGCTTATCCCAAAGCGGAGGCTTACTTGGCTGCATCATCT 1860
Db 1801 ATGGCGCTTTTACGGCTTATCCCAAAGCGGAGGCTTACTTGGCTGCATCATCT 1860
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Db 1861 AGCTCTCAGGCGGCGGACAGGACAGGTCCAGGGGAGGTCGAAGTGTCTCCACCGCA 1920
QY 1921 ACACAAATCTTCTGGCGACCTGCGTCAATGSCGTGTGTGGAGTCTATCATGTTGCC 1980
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QY 2221 GGCGGTCCTGCTCTGCGGCGAGCTGTGGGCACTTTTCGGGCTCGCGGTGCG 2280
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Db 2401 GCCCATCTACGCCCCCTACTGCTAGCGCAGAGCACTAAGGTGCCGCTGGTATGCA 2460
Qy 2461 GCCAAGGGTATAAGGTGCTTCTCTGAACCCGTCGTCGCCGCCACCTAGTTTCGGG 2520
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Qy 2641 TCTGGGGGGCCCTATGACATCATATATATGATGAGTGCACCTCACTGACTCGACCACT 2700
Db 2641 TCTGGGGGGCCCTATGACATCATATATATGATGAGTGCACCTCACTGACTCGACCACT 2700
Qy 2701 ATCTTGGGCATCGGCACAGTCTGGACCAAGCGGAGACGCTGGAGCGGACTCGTCGTG 2760
Db 2701 ATCTTGGGCATCGGCACAGTCTGGACCAAGCGGAGACGCTGGAGCGGACTCGTCGTG 2760
Qy 2761 CTGCGCACGCTACGCTCCGCGATCGGTCAACGTCGCACATCCAAACATCGAGGAGGTG 2820
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Qy 2821 GCTCTGTCAGCACTGAGGAAATCCCTTTTATGGCAAGGCAATCCCGATCGAGACCATC 2880
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Qy 2881 AAGGGGGGAGGACCTTCTGCTGCAATCCAGAGGAATGATGAGCTCGCGCG 2940
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Qy 3001 ATACCAACTAGCGAGAGCGTCAATGCTGTAGCAATATACCGAGAGTGCACCTTACC 3060
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Db 3121 CTGGACCCGACCTTCAACATTTAGAGAGGACGCTGTCACAGACGCGGTGTCAGCTCG 3180
Qy 3181 CAGCGCGAGGAGGAGCTGTTAGGGGAGGATGGGATTTACAGTTTGTGACTCCAGGA 3240
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Db 4021 TGGAAATTCATCAGCGGATACAAATATTTAGCAGGCTTGTCCACTGCTGCTGCGCAACCC 4080
Qy 4081 GCGATAGCATCACTGATGGCATTCACAGCTCTATCACGCGGCTTACACCCCAACAT 4140
Db 4081 GCGATAGCATCACTGATGGCATTCACAGCTCTATCACGCGGCTTACACCCCAACAT 4140
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Qy 4321 TTTTAAAGTTCATGAGCGGAGATGCCCTCCACCGAGGACCTGTTTAACTTCTCCCTGT 4380
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Qy 4501 GGTAAACAGCTCTCCCGGACGACTATGTGCTGAGAGGAGCGCTCAGCAGGTGCTACT 4560
Db 4501 GGTAAACAGCTCTCCCGGACGACTATGTGCTGAGAGGAGCGCTCAGCAGGTGCTACT 4560
Qy 4561 CAGATCCTCTTCTAGTCTTACCATCACTCAGCTGCTGAGAGGCTTCCAGAGTGCATCAAC 4620
Db 4561 CAGATCCTCTTCTAGTCTTACCATCACTCAGCTGCTGAGAGGCTTCCAGAGTGCATCAAC 4620

Db	6781	ACTAATTTCTAAGGCGAGAACTGCGGCTATCCCGGTGCGCGAGCGGTGTACTGACG	6840
Qy	6841	ACCAGTGGGTAAATACCCCTCATGTCTTACTTGAAGCGCGCTGCGGCTGTGAGTGGC	6900
Db	6841	ACCAGTGGGTAAATACCCCTCATGTCTTACTTGAAGCGCGCTGCGGCTGTGAGTGGC	6900
Qy	6901	AGCTCCAGGACTGACGATGCTCGTATGCGGAGGACCTTGTGTTATCTGTGAAGC	6960
Db	6901	AGCTCCAGGACTGACGATGCTCGTATGCGGAGGACCTTGTGTTATCTGTGAAGC	6960
Qy	6961	GCGGACCCAGAGGACGAGCGACCTTACGCGGCTTACGAGGCTATGACTAGATAC	7020
Db	6961	GCGGACCCAGAGGACGAGCGACCTTACGCGGCTTACGAGGCTATGACTAGATAC	7020
Qy	7021	TCTGCCCCCTTGGGACCCGCCAAACAGAAATACGATTGAGTGTGATAACATATGC	7080
Db	7021	TCTGCCCCCTTGGGACCCGCCAAACAGAAATACGATTGAGTGTGATAACATATGC	7080
Qy	7081	TCTTCAATGTGTGAGTGGCGACGATGCTGGAAGAGGTGTACTATCTCACCCGT	7140
Db	7081	TCTTCAATGTGTGAGTGGCGACGATGCTGGAAGAGGTGTACTATCTCACCCGT	7140
Qy	7141	GACCCACACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	7989	100.0	7989	6	AR406043 Sequence
3	7989	100.0	7989	6	AX036255 Sequence
4	7989	100.0	7989	12	AJ242652 Hepatitis
5	7967	99.7	8001	6	AR406042 Sequence
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ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO2059321.
ACCESSION AX739972
VERSION AX739972.1 GI:30519246
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS de Francesco, R., Migliaccio, G. and Paonessa, G.
TITLE Hepatitis C virus replicons and replicon enhanced cells
JOURNAL Patent: WO 02059321-A 3 01-AUG-2002;
ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
(IT)

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
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DB 61 TCTTCAGCGAGAAAGCGTTAGCCATGCGTGTAGTGTGCTGAGTGTGCTGAGCTCCAGGAC 120
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DB 121 CCCCCCTCCCGGAGAGCCATAGTGTGTCGGGAACCGGTGAGTACACCGGAATTGCCAG 180
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Qy	5161	ACATTCCTGTGCGGCTCAATCAATACCTGTGGTGCACAGCTCCCATCGAGCGCCGAA	5220
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Qy	5281	GCTAAGCGTAGCTGGCAGGGATCTCCCGCTCTTGGCGAGTCACTAGCTAGCCAG	5340
Db	5281	GCTAAGCGTAGCTGGCAGGGATCTCCCGCTCTTGGCGAGTCACTAGCTAGCCAG	5340
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Qy	5461	TCAGAAATTAAGTATGATTTTGAATCTTTCAGCGCTCCAGCGGAGGATGAG	5520
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AUTHORS Bartenschlager,R.
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VERSION AX036255.1 GI:11225871
KEYWORDS
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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FEATURES
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1741 AACGCTAGGCCCCCGAACCACCGGACGCTGTTTCTTTGAAAAACACGATATACC 1800
1741 AACGCTAGGCCCCCGAACCACCGGACGCTGTTTCTTTGAAAAACACGATATACC 1800
1801 ATGGGCGCTATTAGGCGCTACTCCAAACAGACGCGAGGCGCTACTTGGCTGATCATCACT 1860
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1921 ACACAATCTTTCTCGGACCTGCGCTCAATGGCGTGTGTGGACTGCTCTATCATGCTGCC 1980
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2101 GGCAGCTCGGACCTTTACTTGGTACAGAGGATGCGGATGTCATTTCCGCTGCGCGCGG 2160
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2161 GGCACAGCAGGGGAGCTACTCTCCCGGCGCGCTCTCCTACTTGAAGGCTCTTTCG 2220
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2221 GGCCTCACCTGCTCGCCCTCGGCGCACGCTGTGGCATCTTTTCGGGCTGCGGTGTC 2280
2281 ACCGAGGGGTTGGAAGGCGGTGGACTTTGTACCCGCTCGAGTCTATGGAAACCACTATG 2340
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3841 GATGAGTGAAGAGTGCCTTACACCTTCCCTTACATCGAACAGGAGATGACGCTCGCC 3900
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QY	3901	GAACAAATCAACAGAGCAATCGGGTGTGCGAAACAGCCACCAAGAGCGGAGCT	3960	QY	4981	GCTGTGAGGAGTACGTGAGGTTACGGGGTGGGGATTTCCACTACGTGACGGCATG	5040
Db	3901	GAACAAATCAACAGAGCAATCGGGTGTGCGAAACAGCCACCAAGAGCGGAGCT	3960	Db	4981	GCTGTGAGGAGTACGTGAGGTTACGGGGTGGGGATTTCCACTACGTGACGGCATG	5040
QY	3961	GCTGTCCCGTGGTGAATCCAAAGTGGCGGACCTCGAAGCCCTTCTGGGCGAAGCATATG	4020	QY	5041	ACCACTGACAAAGTGGCCCGTGTCAAGTTCCGGCCCCCGAAATTTCTTCAAGAAATG	5100
Db	3961	GCTGTCCCGTGGTGAATCCAAAGTGGCGGACCTCGAAGCCCTTCTGGGCGAAGCATATG	4020	Db	5041	ACCACTGACAAAGTGGCCCGTGTCAAGTTCCGGCCCCCGAAATTTCTTCAAGAAATG	5100
QY	4021	TGGAATTTTCATCAGCGCGGATACAATATTTAGCAGGCTTGTCACTCTGCTGCGCAACCC	4080	QY	5101	GATGGGTGCGGTGACAGGTACGCTCCAGCGTGCACACCCCTCTACGGGAGGAGTC	5160
Db	4021	TGGAATTTTCATCAGCGCGGATACAATATTTAGCAGGCTTGTCACTCTGCTGCGCAACCC	4080	Db	5101	GATGGGTGCGGTGACAGGTACGCTCCAGCGTGCACACCCCTCTACGGGAGGAGTC	5160
QY	4081	GGATAGCATCACTGATGGATTCACAGCTCTATCACCAGCCGCTCACCACCAACAT	4140	QY	5161	ACATTCCTCGTGGGCTCAATCAATACCTGTTGGTTCAGCTCCCATCGAGCCCGAA	5220
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QY	4141	ACCTCTCTTTAAACATCTGGGGGATGGTGGCGCCGCAACTTGTCTCTCCAGGCT	4200	QY	5221	CGGAGTACGAGTGTCTCTTCCATGCTCACCGACCCCTCCACATTTACGGCGGAGACG	5280
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QY	4201	GCTTCTGCTTTCTAGCGCGGATCGCTGAGCGGCTTGTGGCAGCATAGGCTTTGG	4260	QY	5281	GCTAACGTAGGTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
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QY	4381	ATCCTCTCTCTGCGCGCTTAGTCTGCGGCTGTGCGGAGCGATCTGCTGCGGAC	4440	QY	5521	AGGAAATAGGTAGTAAATTTGGACTCTTTGAGCTCTTCCAGCGGTCCTCAAGCGGAGGATGAG	5580
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QY	4561	CAGATCTCTCTAGTCTTACATCACTCAGCTGCTGAAGAGGCTTCAACAGTGAATCAAC	4620	QY	5701	CCTCACGGAGGAGGAGACGGTTGCTGTCAGAACTCTACCGTGTCTTCTGCGCTTGGCG	5760
Db	4561	CAGATCTCTCTAGTCTTACATCACTCAGCTGCTGAAGAGGCTTCAACAGTGAATCAAC	4620	Db	5701	CCTCACGGAGGAGGAGACGGTTGCTGTCAGAACTCTACCGTGTCTTCTGCGCTTGGCG	5760
QY	4621	GAGGACTGCTCCAGCCATGCTCGGCTCGTGGCTAAGAGATGTTTGGATGGATATGC	4680	QY	5761	GAGTCTGCGCAAAAGACCTTCGCGAGCTCCGAATCGTGGCGCTGCGAGCGGCACGCGCA	5820
Db	4621	GAGGACTGCTCCAGCCATGCTCGGCTCGTGGCTAAGAGATGTTTGGATGGATATGC	4680	Db	5761	GAGTCTGCGCAAAAGACCTTCGCGAGCTCCGAATCGTGGCGCTGCGAGCGGCACGCGCA	5820
QY	4681	ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGTCCCTGCGCGATTTGCCGGA	4740	QY	5821	ACGGCTCTCTCTGACAGCCCTTCGACGACGCGGATCCGAGCTTGAAGTTCGATC	5880
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AR406042
LOCUS AR406042 8001 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6630343.
ACCESSION AR406042
VERSION AR406042.1 GI:40155169
KEYWORDS SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 8001)
TITLE Bartenschlager,R.
Hepatitis C virus culture system
JOURNAL Patent: US 6630343-A 7 07-OCT-2003;

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Best Local Similarity	99.9%;	Pred. No. 0;
Matches 7989;	Conservative 0;	Mismatches 0; Indels 12; Gaps 1;
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DB	1	GCCAGCCCCGATTTGGGGCGACACTCCACCATAGATCACTCCCTCTGTGAGGAACACTAGT 60
QY	61	TCCTTCAGCAGAAAGCGTCTAGCCATGGCGCTTAGTAGAGTGTCGTGACGCTCCAGGAC 120
DB	61	TCCTTCAGCAGAAAGCGTCTAGCCATGGCGCTTAGTAGAGTGTCGTGACGCTCCAGGAC 120
QY	121	CCCCCTCCCGGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
DB	121	CCCCCTCCCGGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
QY	181	GACGACCGGTCCTTTCTTGGAATCAACCCGCTCAATGCCTGGAGATTGGGCGTGCCTCC 240
DB	181	GACGACCGGTCCTTTCTTGGAATCAACCCGCTCAATGCCTGGAGATTGGGCGTGCCTCC 240
QY	241	GCAGACTGTCTAGCGAGTAGTGTGGGTTCGGAAGGCCCTTGTGTAAGTCTGCTGATAGG 300
DB	241	GCAGACTGTCTAGCGAGTAGTGTGGGTTCGGAAGGCCCTTGTGTAAGTCTGCTGATAGG 300
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DB	301	GTGCTTGCAGTGCCTCCGGGAGTCTCGTAGACCGTGCACATGAGCAGCAATCCTAAAC 360
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DB	361	CTCAAGAAAAACCAAAACCAACAGGCGCGCCATGATTGAACAAGATGATGTC 420
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DB	721	CTCTCTCCGAGAAAGTATCCATATGCTGGCTGATGCAATGCGGCGGTGATACGCTTGATC 780
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QY	1249	AACGTTACTGGCGGAAGCGCTTGGAAATAGGCGCGGTGTGCTTTGTCTATATGTTATT 1308
DB	1261	AACGTTACTGGCGGAAGCGCTTGGAAATAGGCGCGGTGTGCTTTGTCTATATGTTATT 1320
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QY	1369	ACGAGCATTCCTTAGGGTCTTTCCCTCTCGCAAGGAATGCAAGTCTGTTGAATGTC 1428
DB	1381	ACGAGCATTCCTTAGGGTCTTTCCCTCTCGCAAGGAATGCAAGTCTGTTGAATGTC 1440
QY	1429	GTGAAGGAAGCAGTCTCTCTGGAAGCTTCTTGAAGCAAAACAACGTCGTAGGACCTT 1488
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DB	1681	GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTACATGTTTAG 1740
QY	1729	TCGAGGTTAAAAACGCTTAGGCGCGCGGACCAACCGGAGCGTGTCTTCTTTGAAAAA 1788
DB	1741	TCGAGGTTAAAAACGCTTAGGCGCGCGGACCAACCGGAGCGTGTCTTCTTTGAAAAA 1800
QY	1789	CACGATAAATACCATGGCGCTATTACGGCGCTACTTCCCAACAGACGCGAGGCTACTTGGC 1848
DB	1801	CACGATAAATACCATGGCGCTATTACGGCGCTACTTCCCAACAGACGCGAGGCTACTTGGC 1860
QY	1849	TGCATCATCTAGCTTCAAGCGCGGACAGGAACCAAGTCTGAGGGGAGGTCCAAGTG 1908
DB	1861	TGCATCATCTAGCTTCAAGCGCGGACAGGAACCAAGTCTGAGGGGAGGTCCAAGTG 1920
QY	1909	GTCTCCACCGCAACACAATCTTCTTCGCGACTGCGTCAATGCGTGTCTTGCAGCTGTC 1968
DB	1921	GTCTCCACCGCAACACAATCTTCTTCGCGACTGCGTCAATGCGTGTCTTGCAGCTGTC 1980
QY	1969	TATCATGTGTCGGCTCAAAAGACCTTTCCGCGCGCCAAAGGGCCCAATCACCACAAATGAC 2028
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Dd	4561	GCACGTGTCACTCAGATCTCTCTAGTCTTACCATCACTCAGCTGTCTGAAGAGCTTAC	4620	Qy	5689	CCTCCGATACCACTCCACGGAAGAGAGAGCGGTTGTCTGTCTCAGNATCTACCGTGTCT	5748
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Dd	4741	CGATTGCGGAGTCCCTCTTCTCATGTCAACGCTGGGTACAAAGGAGTCTGGCGGGGC	4800	Qy	5869	GTTGAGTGTACTCTCTCATGCCCCCTTGTAGGGGAGCGGGGATCCCGATCTCAGC	5928
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DEFINITION Sequence 3 from Patent EP1043399.
ACCESSION AX036254
VERSION AX036254.1 GI:11225870
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Bartenschlager R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 3 11-OCT-2000;
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Db 2701 GACTCGACCATATCTTCGGGATCGGCATCGGCATCGGCATCGGCATCGGCATCGGCAT 2760
QY 2749 CGACTCGTTCGTGCTCGGCATCGGCATCGGCATCGGCATCGGCATCGGCATCGGCAT 2808
Db 2761 CGACTCGTTCGTGCTCGGCATCGGCATCGGCATCGGCATCGGCATCGGCATCGGCAT 2820
QY 2809 ATCGAGGAGTGGCTCTGTCAGACCTGGAGAAATCCCTTTTATGGCAAGCCATCCCC 2868
Db 2821 ATCGAGGAGTGGCTCTGTCAGACCTGGAGAAATCCCTTTTATGGCAAGCCATCCCC 2880
QY 2869 ATCGAGACCATCAAGGGGGGAGGACCTCATTTCTGCCATTCCTCAAGAGAAATGAT 2928
Db 2881 ATCGAGACCATCAAGGGGGGAGGACCTCATTTCTGCCATTCCTCAAGAGAAATGAT 2940
QY 2929 GAGTTCGCCCCGAAAGTGTCCGCGCTCGGACTCAATGCTGTAGCATATTAACGGGGCTT 2988
Db 2941 GAGTTCGCCCCGAAAGTGTCCGCGCTCGGACTCAATGCTGTAGCATATTAACGGGGCTT 3000
QY 2989 GATGTTTCGTCATACCAACTAGCGGAGCTCAITGTCTGTAGCAACGAGCGCTCTAATG 3048
Db 3001 GATGTTTCGTCATACCAACTAGCGGAGCTCAITGTCTGTAGCAACGAGCGCTCTAATG 3060
QY 3049 ACCGGCTTTACCGGCTATTCGATCAGTATCGATCGATATCATGTGTACCCAGACA 3108
Db 3061 ACCGGCTTTACCGGCTATTCGATCAGTATCGATCGATATCATGTGTACCCAGACA 3120
QY 3109 GTCGACTTCAGCTGACCGGCTTCAACATTCGAGCGGAGCGGCTGTCACCGAGCGG 3168
Db 3121 GTCGACTTCAGCTGACCGGCTTCAACATTCGAGCGGAGCGGCTGTCACCGAGCGG 3180

QY	7549	AGTACCTCTTCAACTGGGCACTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCG	7608
DB	7561	AGTACCTCTTCAACTGGGCACTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCG	7620
QY	7609	TCCAGTTGGATTATTCAGCTGGTTCGTTGCTGTTACAGCGGGGAGACATATATCAC	7668
DB	7621	TCCAGTTGGATTATTCAGCTGGTTCGTTGCTGTTACAGCGGGGAGACATATATCAC	7680
QY	7669	AGCTGTCTGTCGCCGACCCCGCTGGTTCATGTGGTGCCTACTCTCTCTCTAGGG	7728
DB	7681	AGCTGTCTGTCGCCGACCCCGCTGGTTCATGTGGTGCCTACTCTCTCTCTAGGG	7740
QY	7729	GTAGGCATCTATCTACTCCCAACCCGATCAAGCGGGAGCTAAACACTCCAGGCCAATAGG	7788
DB	7741	GTAGGCATCTATCTACTCCCAACCCGATCAAGCGGGAGCTAAACACTCCAGGCCAATAGG	7800
QY	7789	CCATCTCTGTTTTTCCCTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	7848
DB	7801	CCATCTCTGTTTTTCCCTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	7860
QY	7849	TTTTTCTCTTTTTTTTCCCTTTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCTTTAGC	7908
DB	7861	TTTTTCTCTTTTTTTTCCCTTTTTTTTCTTTTTTTCTTTTTTTCTTTTTTTCTTTAGC	7920
QY	7909	CCTAGTCACGGCTAGCTGTCAAAAGTCCGCTGAGCCGCTTGACTGCGAGAGTCTGATAC	7968
DB	7921	CCTAGTCACGGCTAGCTGTCAAAAGTCCGCTGAGCCGCTTGACTGCGAGAGTCTGATAC	7980
QY	7969	TGGCTCTCTGCGAGATCAAGT 7989	
DB	7981	TGGCTCTCTGCGAGATCAAGT 8001	
RESULT 8			
AR406047			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
ORIGIN			
Query Match 99.5%; Score 7949.4; DB 6; Length 8001;			
Best Local Similarity 99.7%; Pred. No. 0;			
Matches 7978; Conservative 11; Mismatches 12; Gaps 1;			
QY	1	GCCAGCCCCGATTGGGGCGACATCCACCATAGATCACTCCCTGTGAGGAACTACTG	60
DB	1	GCCAGCCCCGATTGGGGCGACATCCACCATAGATCACTCCCTGTGAGGAACTACTG	60
QY	61	TCCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGCTGACGCTCCAGAC	120
DB	61	TCCTTCAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGCTGACGCTCCAGAC	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATGGCCAG	180
DB	121	CCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATGGCCAG	180
QY	181	GAGCAGCGGTCTCTTTCTTGATCAACCGCTCAATGCTGGAGATTTGGGCGTGCCTCC	240
DB	181	GAGCAGCGGTCTCTTTCTTGATCAACCGCTCAATGCTGGAGATTTGGGCGTGCCTCC	240

1309 TCCACGATATTCGCGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTCTTTG 1368
1321 TCCACGATATTCGCGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTCTTTG 1380
1369 ACGAGCATTCCTTAGGGTCTTTCCCTCTCGCCAAAGGAATCAAGGTCTGTGAATGTC 1428
1381 ACGAGCATTCCTTAGGGTCTTTCCCTCTCGCCAAAGGAATCAAGGTCTGTGAATGTC 1440
1429 GTGAAGGAGCAGTTCCTCTGGAAGCTTTCTTGAAGACAAACACGTCTGTAGCGACCTTT 1488
1441 GTGAAGGAGCAGTTCCTCTGGAAGCTTTCTTGAAGACAAACACGTCTGTAGCGACCTTT 1500
1489 TGCAGGACGCGAAGCCCGCCACTCGCGACAGGTGCTCTGCGGCAAAAGCCACGTGTA 1548
1501 TGCAGGACGCGAAGCCCGCCACTCGCGACAGGTGCTCTGCGGCAAAAGCCACGTGTA 1560
1549 TAAGATACACCTGCAAGAGCGGCAACCCCGCCACTCGCGACAGGTGCTCTGCGGCAAAAGCCACGTGTA 1608
1561 TAAGATACACCTGCAAGAGCGGCAACCCCGCCACTCGCGACAGGTGCTCTGCGGCAAAAGCCACGTGTA 1620
1609 GAAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAAAGGGGCTGAAGGATGCCCGAGAAG 1668
1621 GAAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAAAGGGGCTGAAGGATGCCCGAGAAG 1680
1669 GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCAATGTTTACATGTGTTTAG 1728
1681 GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCAATGTTTACATGTGTTTAG 1740
1729 TCGAGGTTAAAAACGCTAGGCCCCCGAAGCCAGCGGAGCTGTTTCCCTTTGAAAAA 1788
1741 TCGAGGTTAAAAACGCTAGGCCCCCGAAGCCAGCGGAGCTGTTTCCCTTTGAAAAA 1800
1789 CACGATTAATCCATGGCGCTTATACGSCCTACTCCCAACAGACGCGAGGCTACTTGGC 1848
1801 CACGATTAATCCATGGCGCTTATACGSCCTACTCCCAACAGACGCGAGGCTACTTGGC 1860
1849 TGCATCATCTAGCTCAGAGCGGGGACAGGAACAGAGTCGAGGGGAGGTCCAAAGTG 1908
1861 TGCATCATCTAGCTCAGAGCGGGGACAGGAACAGAGTCGAGGGGAGGTCCAAAGTG 1920
1909 GTCTCCACCGCAACACAACTTTCTCGCGACCTGCGTCAATGGCGTGTGTGACATGTC 1968
1921 GTCTCCACCGCAACACAACTTTCTCGCGACCTGCGTCAATGGCGTGTGTGACATGTC 1980
1969 TATCATGGTCGGCTCAAGAGACCTTTGCGGCGCCAAAGGGCCCAATCACCCAAATGTAC 2028
1981 TATCATGGTCGGCTCAAGAGACCTTTGCGGCGCCAAAGGGCCCAATCACCCAAATGTAC 2040
2029 ACCAATGTGACACGAGACCTGTCGGTGGGAAGCGCCCCCGGGCGCGTTCCTTGACA 2088
2041 ACCAATGTGACACGAGACCTGTCGGTGGGAAGCGCCCCCGGGCGCGTTCCTTGACA 2100
2089 CCATGCACTTCGGCGAGCTCGGACCTTTACTTGTGTACAGGAGATGCGGATGTCATTCCG 2148
2101 CCATGCACTTCGGCGAGCTCGGACCTTTACTTGTGTACAGGAGATGCGGATGTCATTCCG 2160
2149 GTGGCGGGCGGGCGACAGCAGGGGAGCTACTTCTCCCGGAGCGCTCTCTACTTG 2208
2161 GTGGCGGGCGGGCGACAGCAGGGGAGCTACTTCTCCCGGAGCGCTCTCTACTTG 2220
2209 AAGGGCTCTTCGGGGCGGTTCACATGCTCTGCGCTCGGGGACGCTGTGGGCACTTTTCG 2268
2221 AAGGGCTCTTCGGGGCGGTTCACATGCTCTGCGCTCGGGGACGCTGTGGGCACTTTTCG 2280
2269 GCTGCGGTGTGCACCCGAGGGGTTGCAAGCGGTGGACCTTTGTACCCGTGAGTCTATG 2328
2281 GCTGCGGTGTGCACCCGAGGGGTTGCAAGCGGTGGACCTTTGTACCCGTGAGTCTATG 2340
2329 GAAACCACTATGCGGTCCCCTGCTTTCAGCGCAAACTCGTCCCTTCGCGCGTACCGCAG 2388
2341 GAAACCACTATGCGGTCCCCTGCTTTCAGCGCAAACTCGTCCCTTCGCGCGTACCGCAG 2400
2389 ACATTCAGGTGGCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGG 2448

2401 ACAATTCAGGTGGCCCACTACACGCCCTACTGTGTAGCGGCAAGAGCACTAAGGTGCGG 2460
2449 GTCGTATTCGACCCCAAGGGTATAAGGTGTCTTCTTGAAACCCCGTCCCGCGGCACG 2508
2461 GTCGTATTCGACCCCAAGGGTATAAGGTGTCTTCTTGAAACCCCGTCCCGCGGCACG 2520
2509 CTAGGTTCGGGGCGGTATATGTCTAAGGCACATGTGTATCGACCTTAACATCAGAAATCGGG 2568
2521 CTAGGTTCGGGGCGGTATATGTCTAAGGCACATGTGTATCGACCTTAACATCAGAAATCGGG 2580
2569 GTAAGGACCATCACACCGGTGCCCCATCAGTACTCCACTTACCTATGCGCAAGTCTTTCG 2628
2581 GTAAGGACCATCACACCGGTGCCCCATCAGTACTCCACTTACCTATGCGCAAGTCTTTCG 2640
2629 GACGTGTGTTGCTCTGGGGCGCTTATGACATCATATATGTGTAGTGCCACTCAACT 2688
2641 GACGTGTGTTGCTCTGGGGCGCTTATGACATCATATATGTGTAGTGCCACTCAACT 2700
2689 GACTCGACCATCTCTGGGCATCGGCACAGTCTTGGAACGAAGCGGAGCGCTGGAGCG 2748
2701 GACTCGACCATCTCTGGGCATCGGCACAGTCTTGGAACGAAGCGGAGCGCTGGAGCG 2760
2749 CGACTCGTGTGCTCGCCACCGCTACGCTCGGGATCGGTCAAGCGGAGCGCTGGAGCG 2808
2761 CGACTCGTGTGCTCGCCACCGCTACGCTCGGGATCGGTCAAGCGGAGCGCTGGAGCG 2820
2809 ATCAGAGGTGGTCTCTGTCACGACTCGGAAATCCCTTTTATGGAAGCCATCCCC 2868
2821 ATCAGAGGTGGTCTCTGTCACGACTCGGAAATCCCTTTTATGGAAGCCATCCCC 2880
2869 ATCAGAGCATCAAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATGTGAT 2928
2881 ATCAGAGCATCAAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATGTGAT 2940
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2941 GAGTCTCGCGGAAAGTGTCTCGGCTCGGACTCAATGCTGTAGCATATACCGGGGCTT 3000
2989 GATGTATCCGTCATPACCAACTTAGCGGAGAGCTCATTTCTGTAGCAACGAGCTCTAATG 3048
3001 GATGTATCCGTCATPACCAACTTAGCGGAGAGCTCATTTCTGTAGCAACGAGCTCTAATG 3060
3049 ACGGGCTTTACCGCGATTTTCTGACTGATGCAATACATGTGTACCCAGACA 3108
3061 ACGGGCTTTACCGCGATTTTCTGACTGATGCAATACATGTGTACCCAGACA 3120
3109 GTGCACTTCAGCTTGGACCCGACCTTCACCATTTGAGACGACCGTGGCCACAGAGCGG 3168
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3169 GTGTACGCTTCGAGCGGCGAGGACGAGTCTGTAGGGGAGGATGGGCAATTTACAGGTTT 3228
3181 GTGTACGCTTCGAGCGGCGAGGACGAGTCTGTAGGGGAGGATGGGCAATTTACAGGTTT 3240
3229 GTGACTTCAGGAGAAACGGCCCTCGGGCATGTTGCAATTCCTCGTCTGTGCGAGTGTAT 3288
3241 GTGACTTCAGGAGAAACGGCCCTCGGGCATGTTGCAATTCCTCGTCTGTGCGAGTGTAT 3300
3289 GACCGGGCTGTCTTGTGTACGAGCTCAGCCCGCGAGACCTCAGTTAGTTTCGGGCT 3348
3301 GACCGGGCTGTCTTGTGTACGAGCTCAGCCCGCGAGACCTCAGTTAGTTTCGGGCT 3360
3349 TACCTAAACACACAGGGTTGCCGCTCTGCCAGAACCACTGTGGAGTCTGGGAGAGGTC 3408
3361 TACCTAAACACACAGGGTTGCCGCTCTGCCAGAACCACTGTGGAGTCTGGGAGAGGTC 3420
3409 TTTTACAGGCTCACCCACATAGAGCCCAATTTCTGTCCAGACTAAGCAGGAGGAGAC 3468
3421 TTTTACAGGCTCACCCACATAGAGCCCAATTTCTGTCCAGACTAAGCAGGAGGAGAC 3480
3469 AACTTCCCTTACTGTGTAGCATACAGGCTCAGTGTGTGCGGAGGCTCAGGCTCACCT 3528

3481	AACTTCCCCTACCTGGTAGCATACACAGGCTACGGTGTGCGCCAGGGGTCAAGGCTCCACCT	3540
3529	CCATCTGTGGGACCAATGTGGAAAGTGTCTCATACGGCTAAAGCCCTACGCTGCACGGGCCA	3588
3541	CCATCTGTGGACCAATGTGGAAAGTGTCTCATACGGCTAAAGCCCTACGCTGCACGGGCCA	3600
3589	ACGCCCCCTGCTGTATAGGCTGGGAGCCGTTCAAAACGAGGTTACTTACACACACCCCATTA	3648
3601	ACGCCCCCTGCTGTATAGGCTGGGAGCCGTTCAAAACGAGGTTACTTACACACACCCCATTA	3660
3649	ACCAATATACATATGCATATGCATATGCCTGTACCTGTGAGGTCTGACAGCACCTGGGTG	3708
3661	ACCAATATATCATATGCATATGCCTGTACCTGTGAGGTCTGACAGCACCTGGGTG	3720
3709	CTGGTAGGCGAGTCTCCTAGCAGCTCTGGCGGTATTGCTGTACAAACAGGCGAGGTGCTC	3768
3721	CTGGTAGGCGAGTCTCCTAGCAGCTCTGGCGGTATTGCTGTACAAACAGGCGAGGTGCTC	3780
3769	ATTGTGGGCAAGGATCATCTTTGTCCGAAACCGCGGCATCATTTCCCGACAGGAGTCTCT	3828
3781	ATTGTGGGCAAGGATCATCTTTGTCCGAAACCGCGGCATCATTTCCCGACAGGAGTCTCT	3840
3829	TACCGGAGGTTCCATATGATATGAGTAGTGGCTCACACTCCCTTACATCGAAACAGGGA	3888
3841	TACCGGAGGTTCCATATGATATGAGTAGTGGCTCACACTCCCTTACATCGAAACAGGGA	3900
3889	ATGCAGCTCCGCGAACCAATTAACACGAGGCAATCGGTTGCTGTCAACACAGCCACCAAG	3948
3901	ATGCAGCTCCGCGAACCAATTAACACGAGGCAATCGGTTGCTGTCAACACAGCCACCAAG	3960
3949	CAAGCGGAGGTGCTGTCTCCGTTGGTGGAAATCAAGTGGCGGACCTCGAAAGCTTCTGG	4008
3961	CAAGCGGAGGTGCTGTCTCCGTTGGTGGAAATCAAGTGGCGGACCTCGAAAGCTTCTGG	4020
4009	CGAAGCATATGTGGAAATTTTCATCAGCGGATACAAATTTAGCAGGCTTGTCCACTCTG	4068
4021	CGAAGCATATGTGGAAATTTTCATCAGCGGATACAAATTTAGCAGGCTTGTCCACTCTG	4080
4069	CCTGCGACCCCGGATAGCATCACTATGGCATTTACAGCCCTTATCACAGCCCGCTC	4128
4081	CCTGCGACCCCGGATAGCATCACTATGGCATTTACAGCCCTTATCACAGCCCGCTC	4140
4129	ACCACCCCAACATACCCCTCTCTTTAAACATCCTGGGGGATGGTGGCGGCCAACTTGCT	4188
4141	ACCACCCCAACATACCCCTCTCTTTAAACATCCTGGGGGATGGTGGCGGCCAACTTGCT	4200
4189	CTCCACGCGCTCTCTCTCTTTGCTAGGCGCGGCATCGCTGGAGCGGTGTGGCAGC	4248
4201	CTCCACGCGCTCTCTCTCTTTGCTAGGCGCGGCATCGCTGGAGCGGTGTGGCAGC	4260
4249	ATAGGCTTGGAAAGTCTTGTGATATTTTGGCAGTTATGGAGCAGGGGTGGCAGGC	4308
4261	ATAGGCTTGGAAAGTCTTGTGATATTTTGGCAGTTATGGAGCAGGGGTGGCAGGC	4320
4309	GGGCTCTGGCCCTTTAAAGTTCATATGACGGCGAGATGCCCTCCACCGAGGACCTGGTTAC	4368
4321	GGGCTCTGGCCCTTTAAAGTTCATATGACGGCGAGATGCCCTCCACCGAGGACCTGGTTAC	4380
4369	CTACTCCCTGTCTATCTCTCCCTGGCGCCCTAGTCTGGGGTCTGTGGCAGCGATA	4428
4381	CTACTCCCTGTCTATCTCTCTCCCTGGCGCCCTAGTCTGGGGTCTGTGGCAGCGATA	4440
4429	CTGCGTCCGACGTGGGCCACGGGAGGGGGCTGTGCAGTGGATGAACCCGGCTGATAGC	4488
4441	CTGCGTCCGACGTGGGCCACGGGAGGGGGCTGTGCAGTGGATGAACCCGGCTGATAGC	4500
4489	TTCCGCTTCGGGGGTAAACCAAGTCTCCGCCACGCACTATGTGCTGTAGAGGACGCTGCA	4548
4501	TTCCGCTTCGGGGGTAAACCAAGTCTCCGCCACGCACTATGTGCTGTAGAGGACGCTGCA	4560
4549	GCACGTGTCACTCAGATCTCTTCTAGTCTTACCATCACTCAGCTGCTCAAGAGGCTTCAC	4608
4561	GCACGTGTCACTCAGATCTCTTCTAGTCTTACCATCACTCAGCTGCTCAAGAGGCTTCAC	4620

QY	4609	CAGTGGATACACGAGGACTGCTCCACGCCATTGCTCCGGCTCGTGGCTAAGACATGTTGG	4668
DB	4621	CAGTGGATACACGAGGACTGCTCCACGCCATTGCTCCGGCTCGTGGCTAAGACATGTTGG	4680
QY	4669	GATTGGATATGCACGGTGTTCAGTGAATTTCAAGACTCGCTCCAGTCCAGCTCTCTGGCGG	4728
DB	4681	GATTGGATAUGCACGGTGTTCAGTGAATTTCAAGACTCGCTCCAGTCCAGCTCTCTGGCGG	4740
QY	4729	CGATTGCCGGAGTCCCTCTTCTCATGTCAACCTGGGTACAAGGGAGCTCTGGCGGGGC	4788
DB	4741	CGATTGCCGGAGTCCCTCTTCTCATGTCAACCTGGGTACAAGGGAGCTCTGGCGGGGC	4800
QY	4789	GACGSCATCATGCAAAACCACTGCCCATGTGGAGCAGATCACCGGACATGTGAAAAAC	4848
DB	4801	GACGSCATCATGCAAAACCACTGCCCATGTGGGSCACAGATCACCGGACATGTGAAAAAC	4860
QY	4849	GGTTCATAGAGATCGTGGGGCTTAGACCTGTAGTAAACAGTGGCATCGAACTTCCCC	4908
DB	4861	GGTTCATAGAGATCGTGGGGCTTAGACCTGTAGTAAACAGTGGCATCGAACTTCCCC	4920
QY	4909	ATTAACGGCTACACACAGGGGCCCTGACGCGCTCCCGGCGCAAAATTTCTAGGGCG	4968
DB	4921	ATTAACGGCTACACACAGGGGCCCTGACGCGCTCCCGGCGCAAAATTTCTAGGGCG	4980
QY	4969	CTGTGCGGGTGGCTGCTGAGGAGTACGTGGAGTTACGGGTGGGGGATTTCCACTAC	5028
DB	4981	CTGTGCGGGTGGCTGCTGAGGAGTACGTGGAGTTACGGGTGGGGGATTTCCACTAC	5040
QY	5029	GTGACGGGATGACACACTGACACAGCTAAAGTGCCTGTGACGTTCCGGCCCCGAATTC	5088
DB	5041	GTGACGGGATGACACACTGACACAGCTAAAGTGCCTGTGACGTTCCGGCCCCGAATTC	5100
QY	5089	TTCACAGAAGTGTGCGGGTGGCTGTCACAGAGTACGCTCCAGCGTCAAAACCCCTCTA	5148
DB	5101	TTCACAGAAGTGTGCGGGTGGCTGTCACAGAGTACGCTCCAGCGTCAAAACCCCTCTA	5160
QY	5149	CGGGAGGAGTCAATTCCTGTGCGGCTCAATCAATPACCTGTTGGGTACAGCTCCCA	5208
DB	5161	CGGGAGGAGTCAATTCCTGTGCGGCTCAATCAATPACCTGTTGGGTACAGCTCCCA	5220
QY	5209	TGGAGCCGAACCGGACGTAGCAGTGTCACTTCCATGTCCAGGACCCCTCCCAATT	5268
DB	5221	TGGAGCCGAACCGGACGTAGCAGTGTCACTTCCATGTCCAGGACCCCTCCCAATT	5280
QY	5269	ACGGCGAGACGGCTAAGCGTAGCGTGCGCAGGGGATCTCCCGCTCTTGGCGAGTCA	5328
DB	5281	ACGGCGAGACGGCTAAGCGTAGCGTGCGCAGGGGATCTCCCGCTTGGCGAGTCA	5340
QY	5329	TCAGCTAGCCAGTGTCTGCGCTTCTTGAAGGCAATGCACTACCGCTCATGACTCC	5388
DB	5341	TCAGCTAGCCAGTGTCTGCGCTTCTTGAAGGCAATGCACTACCGCTCATGACTCC	5400
QY	5389	CCGAGCGCTGACCTCATTCAGGGCCAACTCTCTGTGGCGGACAGGATGGGGGGAACATC	5448
DB	5401	CCGAGCGCTGACCTCATTCAGGGCCAACTCTCTGTGGCGGACAGGATGGGGGGAACATC	5460
QY	5449	ACCGCGTGGAGTCAGAAAAATPAGGTAGTAATTTTGGACTCTTTTCGAGCGCTCCAGCG	5508
DB	5461	ACCGCGTGGAGTCAGAAAAATPAGGTAGTAATTTTGGACTCTTTTCGAGCGCTCCAGCG	5520
QY	5509	GAGGAGATGAGGGGAGTATCCGTTTCCGGCGGAGATCCCTGCGAGGTCCAGGAAATTC	5568
DB	5521	GAGGAGATGAGGGGAGTATCCGTTTCCGGCGGAGATCCCTGCGAGGTCCAGGAAATTC	5580
QY	5569	CCTCGAGCGATGCCCATATGGGCAACGCCCGGATTAACACCTTCACTGTAGAGTCTTGG	5628
DB	5581	CCTCGAGCGATGCCCATATGGGCAACGCCCGGATTAACACCTTCACTGTAGAGTCTTGG	5640
QY	5629	AAGACCCGACTAGTCCCTCCAGTGTACACGGGTCTCAATGCCGCTCCCAAGGCC	5688
DB	5641	AAGACCCGACTAGTCCCTCCAGTGTACACGGGTCTCAATGCCGCTCCCAAGGCC	5700

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Db 1621 GAAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAG 1680
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Db 1801 CACGATATACATGGCGCTATTACGGCTTACTCCAAACAGACGCGAGGCTACTTGGC 1860
QY 1849 TGCATCATCACTAGCTCACAGGCGGGACAGGACAGGCTCGAGGGAGGTCCAAGTG 1908
Db 1861 TGCATCATCACTAGCTCACAGGCGGGACAGGACAGGCTCGAGGGAGGTCCAAGTG 1920
QY 1909 GTCTCCACCGCAACACAATCTTCTTGGCGACCTGCGTCAATGGCGTGTGTGGACTGTC 1968
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QY 1969 TATCATGTCGCGCTCAAGACCTTTCGCGGCCCCAAGGGCCCCAATCACCCAAATGTAC 2028
Db 1981 TATCATGTCGCGCTCAAGACCTTTCGCGGCCCCAAGGGCCCCAATCACCCAAATGTAC 2040
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QY 2629 GACGTTGGTGTCTCTGGGGCGCTATGACATCATATATGTCATGAGTGCCACTCAACT 2688
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QY 1969 TATCATGTGCGGCTCAAGACCCCTTTCGCGCCCAAGGGGCCAATCACCCAAATGTAC 2028
DB 1981 TATCATGTGCGGCTCAAGACCCCTTTCGCGCCCAAGGGGCCAATCACCCAAATGTAC 2040
QY 2029 ACCAATGTGACAGGACCTCGTGGCTGGCAAGGCCCGCCCGGGCGGCTTCCTTGACA 2088
DB 2041 ACCAATGTGACAGGACCTCGTGGCTGGCAAGGCCCGCCCGGGCGGCTTCCTTGACA 2100
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DB 2161 GTGCGCCCGGGGGGACAGAGGGGAGCCCTACTCTCCCCAGGCCCGTCTCTTACTTG 2220
QY 2209 AAGGCTCTTTCGGGCGGTCCATGCTCTGCCCCCTCGGGGACGCTGTGGGACCTTTTCG 2268
DB 2221 AAGGCTCTTTCGGGCGGTCCATGCTCTGCCCCCTCGGGGACGCTGTGGGACCTTTTCG 2280
QY 2269 GCTGCGGTGTCACCCGAGGGGTTGCGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATG 2328
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QY 2329 GAAACCACTATGCGGTTCGCCGTCTTTCAGGACAACTCGTCCCTCCGCGGTACCGGAG 2388
DB 2341 GAAACCACTATGCGGTTCGCCGTCTTTCAGGACAACTCGTCCCTCCGCGGTACCGGAG 2400
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DB 2401 ACATTCAGGTGGGCCATCTACGCCCTACTGTTACGACAACTCGTCCCTCCGCGGTACCGGAG 2460
QY 2449 GCTGCGTATGACGCCCAAGGGTATAAGGTGCTTGTCTGAACCCGTCGTCGCGGCCACC 2508
DB 2461 GCTGCGTATGACGCCCAAGGGTATAAGGTGCTTGTCTGAACCCGTCGTCGCGGCCACC 2520
QY 2509 CTAGGTTTCGGGGGTTATGTCTAAGGCAATCGGTATCGACCTTAACATCAGAACCGGG 2568
DB 2521 CTAGGTTTCGGGGGTTATGTCTAAGGCAATCGGTATCGACCTTAACATCAGAACCGGG 2580
QY 2569 GTAAGGACCATCACACGGGTGCCCTACGCTACGCTACCTATGGAAGTTCCTTGCC 2628
DB 2581 GTAAGGACCATCACACGGGTGCCCTACGCTACGCTACCTATGGAAGTTCCTTGCC 2640
QY 2629 GACGGTGGTTGCTCTGGGGGCGCTATGACATATAATATGTATGATGTCACCTCAACT 2688
DB 2641 GACGGTGGTTGCTCTGGGGGCGCTATGACATATAATATGTATGATGTCACCTCAACT 2700
QY 2689 GACTCGACCATATCTTGGGGATCGGCACAGTCTTGACCAAGCGGAGCGGCTGGAGCG 2748
DB 2701 GACTCGACCATATCTTGGGGATCGGCACAGTCTTGACCAAGCGGAGCGGCTGGAGCG 2760
QY 2749 CGACTCGTGTGTCGCCACCGCTACGCTCCGGATCGGTACCGTGCACATCCTCAAC 2808
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QY 4069 CTTGGCAACCCCGGATAGCATCTATGAGTGTGCAATTCACAGCTCTATACAGCAGCGCTC 4128
DB 4081 CTTGGCAACCCCGGATAGCATCTATGAGTGTGCAATTCACAGCTCTATACAGCAGCGCTC 4140
QY 4129 ACCACCAACATACCTCTCTGTTTAACTCTTGGGGGATGGGTGGCGGCCCAACTGTCT 4188

Db	4141	ACCAACCAACATACACCTCTCTGTTTAACTCTCGGGGATGGGTGGCGCCCAACTTGT	4200		Db	5221	TGCGGGCCGAACCGGACGTAGCAGTGTCTCACTTCCATGCTCACCGACCCCTCCACATT	5280
Qy	4189	CCTCCAGCGCTGCTTCTGCTTTTCGTAGCGCGCGCATGCTGGAGCGGCTTTGGCAGC	4248		Qy	5269	ACGCGGAGACGGCTAAAGCTAGGCTGGCCAGGGGATCTCCCTCTCTTTGGCCAGTCA	5328
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Qy	4249	ATAGCGCTTGGAAAGTGTCTTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGC	4308		Qy	5329	TCAGCTAGCCAGCTGTCTGGCGCTTCTTTGAAGGCAACATGCACTACCGTCTATGATCC	5388
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Db	4321	GGCTCTGGCTTTAAAGTCTATAGCGCGGATGCTCCACAGGACCTGTTTAAAC	4380		Db	5401	CGGACGCTGACCTCATCGAGGCGAACCTCTGTCGCGCAGAGATGGCGGGAAACATC	5460
Qy	4369	CTACTCCCTGCTATCTCTCCCTTGGCGCTTAGTCTCGGGGTCTGTGCGCAGGATA	4428		Qy	5449	ACCGCGTGGAGTCAGAAAATAAGTAGTAAATTTTGGACTCTTTGAGCGCGTCCAAAGCG	5508
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Db	4561	GCAGTGTCTACTCAGATCTCTTAGTCTTACATCACTCAGCTGTGAAGAGCTTAC	4620		Db	5641	AAGGACCCGCACTACCTCCCTCCAGTGTACAGGGGTGTCATGTCGCGCTGCCAAGGCC	5700
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Db	4741	CGATTGCGGGAGTCCCTTCTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGC	4800		Db	5821	AGCGGACCGCAACGGCTCTCTCTGACAGCCCTTCGACGACGGCGGAGATCCGAC	5880
Qy	4789	GACGGCATATGCAAAACCACTGCGCATGTGGAGCAGACATCACCGACATGTCAAAAAC	4848		Qy	5869	GTTGAGTGTACTCTCTCATGTGCGGGGAGCGGGGATCCCGATCTCAGC	5928
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Qy	4849	GTTTCCATGAGATCGTGGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCGCC	4908		Qy	5929	GACGGCTTGTGCTACCGTAAAGCGAGGAGCTAGTACAGGACGTCGTCGTCGATG	5988
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QY	7129	TATCTCACCCTGACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACAC	7188
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Dd	7861	TTTTCTCCTTTTTTTTTTCCCTTTTTTCTTTTTTCTTTTTTCTTTTGGTGGCTCCATCTTAGC	7920
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Dd	7921	CCTAGTCACGGCTAGCTGTGAAGGTCCTGTAGCGGCTTGACTGCAGAGAGTCTCATAC	7980
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VERSION	AX036257.1	GI:11225873	
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REFERENCE	1		
AUTHORS	Bartenschlager,R.D.		
TITLE	Hepatitis c virus cell culture system		
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	Query Match	99.4%	Score 7947.8	DB 6	Length 8001
	Best Local Similarity	99.7%	Pred. No. 0		
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				Gaps 1	
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Db	1	GCACGCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTCTGTGAGGAAC	CTGTG	60	
QY	61	TCCTTCAGCGAAGCGCTTAGCCATGGCGTTATGATAGTGTGGTGCAGCTCCACGAC		120	

Db	1141	CTCCGATTTCGACGGCATGCGCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGTTAAA	1200
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Db	1381	ACGAGCATTTCTAGGGGTCTTTCCCTCTCGCCAAAGAAATGCAAGTCTGTGAAATGTC	1440
Qy	1429	GTGAAGGAAGCAGTTCTCTGGAAGCTTCTTGAAGACAACACAGTCTGTAGCGACCTT	1488
Db	1441	GTGAAGGAAGCAGTTCTCTGGAAGCTTCTTGAAGACAACACAGTCTGTAGCGACCTT	1500
Qy	1489	TGCAGCAGCGGAACCCCTCCTGCGCAGAGTGCCTCTGCGGCCAAAGACCAACGTTA	1548
Db	1501	TGCAGCAGCGGAACCCCTCCTGCGCAGAGTGCCTCTGCGGCCAAAGACCAACGTTA	1560
Qy	1549	TAAGATACACCTCTCAAAGCGGCACAAACCCAGTGCACCGTTGTAGTTGATGTTG	1608
Db	1561	TAAGATACACCTCTCAAAGCGGCACAAACCCAGTGCACCGTTGTAGTTGATGTTG	1620
Qy	1609	GAAAGAGTCAATGCGTCTCTCAAGGTTTCAACAAAGGGCTGAGGATGCCAAG	1668
Db	1621	GAAAGAGTCAATGCGTCTCTCAAGGTTTCAACAAAGGGCTGAGGATGCCAAG	1680
Qy	1669	GTACCCCATTTGATGGATCTGATCTGGGCTCTCGTGCACATGCTTTACATGTTTAC	1728
Db	1681	GTACCCCATTTGATGGATCTGATCTGGGCTCTCGTGCACATGCTTTACATGTTTAC	1740
Qy	1729	TCGAGGTTAAAAAAGCTTAGGCCCCCGGACCAACGAGGGGCTGTTTCTTTGAAAAA	1788
Db	1741	TCGAGGTTAAAAAAGCTTAGGCCCCCGGACCAACGAGGGGCTGTTTCTTTGAAAAA	1800
Qy	1789	CACGATTAATACATGCGGCTTATACGCTCTACCCCAACAGACGCGAGGCTACTTGGC	1848
Db	1801	CACGATTAATACATGCGGCTTATACGCTCTACCCCAACAGACGCGAGGCTACTTGGC	1860
Qy	1849	TGCATCATCTAGCTCTACAGCGCGGACAGGAACACAGGTCGAGGGGGAGGTCGAAGTG	1908
Db	1861	TGCATCATCTAGCTCTACAGCGCGGACAGGAACACAGGTCGAGGGGGAGGTCGAAGTG	1920
Qy	1909	GTCTCCACCGCAACACATCTTCTGCGGACCTTGTGCGTCAATGCGGTGTGTGACGTC	1968
Db	1921	GTCTCCACCGCAACACATCTTCTGCGGACCTTGTGCGTCAATGCGGTGTGTGACGTC	1980
Qy	1969	TATCATGTTGCGGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTAC	2028
Db	1981	TATCATGTTGCGGCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTAC	2040
Qy	2029	ACCAATGTGACACAGGACCTCTGCGTGTGCAAGCGCCCCCGGGGCGCTTCTTGTACA	2088
Db	2041	ACCAATGTGACACAGGACCTCTGCGTGTGCAAGCGCCCCCGGGGCGCTTCTTGTACA	2100
Qy	2089	CCATGCACTCGGCGAGCTCGGACCTTCTTGTGTGTCAGAGGATGCCGATGTCAITCG	2148
Db	2101	CCATGCACTCGGCGAGCTCGGACCTTCTTGTGTGTCAGAGGATGCCGATGTCAITCG	2160
Qy	2149	GTGCGCGCGGGGCGAGCAGAGGGGAGCTTCTCTCCCGAGCCCGCTCTCTACTTTG	2208
Db	2161	GTGCGCGCGGGGCGAGCAGAGGGGAGCTTCTCTCCCGAGCCCGCTCTCTACTTTG	2220
Qy	2209	AAGGCTCTTTCGGGCGGTCCACTGCTCTGCCCTCGGGGACAGCTGTGGGCACTTTTCG	2268
Db	2221	AAGGCTCTTTCGGGCGGTCCACTGCTCTGCCCTCGGGGACAGCTGTGGGCACTTTTCG	2280

Db	4441	CTGGTCGGCAGCTGGGCCCAGGGAGGGGCTGTGAGTGATGAAACGGCTGATAGCG	4500	5521	GAGGAGGATGAGAGGGAAGTATCCGTTCCGGGGGAGATCCTCGCGAGGTCCAGGAAATTC	5580
Qy	4489	TTCCGTTCCGGGGTAAACACAGCTCTCCCCACGCACTATGCTGCTGAGAGGACGCTGCA	4548	5569	CCTCGAGGATGCCCATATGGGCGACGCCCGGATTAACAACCTTCCACTGTGTAGAGTCTGG	5628
Db	4501	TTCCGTTCCGGGGTAAACACAGCTCTCCCCACGCACTATGCTGCTGAGAGGACGCTGCA	4560	5581	CCTCGAGGATGCCCATATGGGCGACGCCCGGATTAACAACCTTCCACTGTGTAGAGTCTGG	5640
Qy	4549	GCAGTGTCACTCAGATCCCTCTCTAGTCTTACCATCACTCAGCTGCTGAGAGGCTTCAAC	4608	5629	AAGGACCCGGACTAGCTCCCTCAGTGTGTACAGGGTGTCCATTCGCGCTCCGAGGCC	5688
Db	4561	GCAGTGTCACTCAGATCCCTCTCTAGTCTTACCATCACTCAGCTGCTGAGAGGCTTCAAC	4620	5641	AAGGACCCGGACTAGCTCCCTCAGTGTGTACAGGGTGTCCATTCGCGCTCCGAGGCC	5700
Qy	4609	CAGTGGATCAACGAGGACTGCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTGG	4668	5689	CCTCGGATACCACTCCACGGAGGAGGAGCGTGTCTCTGTGAGAAATCTACCGTGTCT	5748
Db	4621	CAGTGGATCAACGAGGACTGCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTGG	4680	5701	CCTCGGATACCACTCCACGGAGGAGGAGCGTGTCTCTGTGAGAAATCTACCGTGTCT	5760
Qy	4669	GATTGGATATGACCGGTGTGACTGATTTCAGAACCTGGCTCAGTCCAGTCTCTGGCG	4728	5749	TTCTGCTTTGGCGGAGCTCGCCAACAAGACCTTTGGGAGCTCCGAAATCTGCGCGCTCGAC	5808
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Qy	4729	CGATTCCGGGAGTCCCTTCTCTCATGTCAACGTGGGTACAGGGAGTCTGGCGGGC	4788	5809	AGCGGACCGGAAACGGCTCTCTGACAGCCCTCCGACAGCGGACCGCGGATCCGAC	5868
Db	4741	CGATTCCGGGAGTCCCTTCTCTCATGTCAACGTGGGTACAGGGAGTCTGGCGGGC	4800	5821	AGCGGACCGGAAACGGCTCTCTGACAGCCCTCCGACAGCGGACCGCGGATCCGAC	5880
Qy	4789	GACGGCATCATCAACACCTGCTCCCATGTGGAGCACAGATCACCGGACATGTGAAAAAC	4848	5869	GTGTAGTCCGTACTCTCTCCATGCCCTTGAAGGGGAGCGCGGGGATCCCGATCTCAGC	5928
Db	4801	GACGGCATCATCAACACCTGCTCCCATGTGGAGCACAGATCACCGGACATGTGAAAAAC	4860	5881	GTGTAGTCCGTACTCTCTCCATGCCCTTGAAGGGGAGCGCGGGGATCCCGATCTCAGC	5940
Qy	4849	GGTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACACGTGGCATGGAACATTC	4908	5929	GACGGGTCTTGGTCTTACCGTAAAGCGGAGGCTGTGTGAGGACGCTGTCTGTCTGATG	5988
Db	4861	GGTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACACGTGGCATGGAACATTC	4920	5941	GACGGGTCTTGGTCTTACCGTAAAGCGGAGGCTGTGTGAGGACGCTGTCTGTCTGATG	6000
Qy	4909	ATTAAACGGGTACACAGGGCCCTTCTGACCGCTCCCGGCGCAATTTCTAGGGG	4968	5989	TCCTACATGAGACGGCCCTGTATCAGCCATGCGCTCGGAGGAAACCAAGCTGCC	6048
Db	4921	ATTAAACGGGTACACAGGGCCCTTCTGACCGCTCCCGGCGCAATTTCTAGGGG	4980	6001	TCCTACATGAGACGGCCCTGTATCAGCCATGCGCTCGGAGGAAACCAAGCTGCC	6060
Qy	4969	CTGTGGGGTGTGCTGAGGAGTACGTGGAGTACGGGGTGGGGATTTCCACTAC	5028	6049	ATCAATGCACTGAGCAACTCTTTGCTCCGTACCAACAATTTGCTGTATGTACAACTCT	6108
Db	4981	CTGTGGGGTGTGCTGAGGAGTACGTGGAGTACGGGGTGGGGATTTCCACTAC	5040	6061	GTCAATGCACTGAGCAACTCTTTGCTCCGTACCAACAATTTGCTGTATGTACAACTCT	6120
Qy	5029	GTGACGGGCAATGACCACTGACAAAGTAAAGTGGCCGTGTGAGGTTCGGCCCGGATTC	5088	6109	CGCAGCGCAAGCTTGGCGCAAGAAAGTCACTTTGACAGACTGTGAGGCTTGGAGCAG	6168
Db	5041	GTGACGGGCAATGACCACTGACAAAGTAAAGTGGCCGTGTGAGGTTCGGCCCGGATTC	5100	6121	CGCAGCGCAAGCTTGGCGCAAGAAAGTCACTTTGACAGACTGTGAGGCTTGGAGCAG	6180
Qy	5089	TTCAAGAGTGTGATGGGTGCGGTTGCAAGGTACGCTCCAGGTGCAACCCCTCTTA	5148	6169	CATACCGGAGCTGTCTCAAGGAGATGAAGCGAAGCGGTCCACAGTTAAGGCTTAACTT	6228
Db	5101	TTCAAGAGTGTGATGGGTGCGGTTGCAAGGTACGCTCCAGGTGCAACCCCTCTTA	5160	6181	CATACCGGAGCTGTCTCAAGGAGATGAAGCGAAGCGGTCCACAGTTAAGGCTTAACTT	6240
Qy	5149	CGGAGGAGGTTCATTTCTGCTGGGCTCAATCAATACCTGTGAGTCAAGCTCCCA	5208	6229	CTATCCGTGGAGGAGCTGTAGCTGACGCCCCCAATTCGGCCAGATCTTAAATTTGGC	6288
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Qy	5209	TGCGAGCCGGAACCGGACGTAGCTGCTACTTCCATGCTACCGACCCCTCCACAT	5268	6289	TATGGGCAAGGACGTCGCGAACCCTATCCAGCAAGCGGCTTAAACATCCGCTCCGTG	6348
Db	5221	TGCGAGCCGGAACCGGACGTAGCTGCTACTTCCATGCTACCGACCCCTCCACAT	5280	6301	TATGGGCAAGGACGTCGCGAACCCTATCCAGCAAGCGGCTTAAACATCCGCTCCGTG	6360
Qy	5269	ACGGGAGAGCGGTAAAGTGGCTGAGGAGGATCTCCCTCTCTGCGGAGCTCA	5328	6349	TGGAAGGACTTGTCTGGAAGACACTGAGACCAATTTGACACCAATCATGCGCAAAAT	6408
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Qy	5329	TCAGTACGAGCTGTCTGCGGCTTCTTGAAGGCAACATGCACTACCCGCTCATGCT	5388	6409	GAGGTTTTCTCGCTCCAAACAGAGAGAGGGGGCGCGAAGCCAGCTTCGCTTATCGATTC	6468
Db	5341	TCAGTACGAGCTGTCTGCGGCTTCTTGAAGGCAACATGCACTACCCGCTCATGCT	5400	6421	GAGGTTTTCTCGCTCCAAACAGAGAGAGGGGGCGCGAAGCCAGCTTCGCTTATCGATTC	6480
Qy	5389	CCGAGCGTGAATCATCGAGGCAACCTCTGTGGCGGAGGAGATGGCGGGAGATC	5448	6469	CCAGATTTGGGGTTCGTTGTGCGAGAAATGGCCCTTTACGATGTTGTTCTCCACCTC	6528
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Qy	5449	ACCGCGTGGAGTCAAGAAATAGTGTATTTTGGACTCTTTTCGAGCCGCTCCAGCG	5508	6529	CCTCAGGCGGTGATGGGCTCTTCAACGATTTCAATACTCTCTCTGGAGAGCGGCTCGAG	6588
Db	5461	ACCGCGTGGAGTCAAGAAATAGTGTATTTTGGACTCTTTTCGAGCCGCTCCAGCG	5520	6541	CCTCAGGCGGTGATGGGCTCTTCAACGATTTCAATACTCTCTCTGGAGAGCGGCTCGAG	6600
Qy	5509	GAGGAGGATGAGAGGGAAGTATCCGTTCCGGCGGAGATCTCTCGGAGGTTCAGGAAATTC	5568	6589	TTCTCGTGTGAATGCTCGGAAAGCGAAGAAATGCCCTATGGGCTTCGCAATATGACACCGC	6648
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QY	6649	TGTTTGA	CTCAACGGTCACTGAGAA	TGACATCCGTTGTGAGGAGTCAATCTACCAATGT	6700
Db	6661	TGTTTGA	CTCAACGGTCACTGAGAA	TGACATCCGTTGTGAGGAGTCAATCTACCAATGT	6720
QY	6709	TGTGACT	TGGCCCCCGAAGCCAGACAGGCCA	TAAGTTCGTCTACAGAGCGGCTTTTACATC	6768
Db	6721	TGTGACT	TGGCCCCCGAAGCCAGACAGGCCA	TAAGTTCGTCTACAGAGCGGCTTTTACATC	6780
QY	6769	GGGGCCCCCTGACTAA	TTCTAAAGGCGAGAACTCGCGCTAT	CGCCGGTCCCGCGGAGC	6828
Db	6781	GGGGCCCCCTGACTAA	TTCTAAAGGCGAGAACTCGCGCTAT	CGCCGGTCCCGCGGAGC	6840
QY	6829	GGTGTACTGACGAC	AGCTGCGGTAATACCCCTACATGTTACT	TGAAGGCGGCTCGCGGC	6888
Db	6841	GGTGTACTGACGAC	AGCTGCGGTAATACCCCTACATGTTACT	TGAAGGCGGCTCGCGGC	6900
QY	6889	TGTCGAGCTCGAAGCT	CCAGGACTGACGAGTCTGATGCGGAGACGACCTTGTGCTT	6948	
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QY	6949	ATCTGTGAAAGCGCGG	GGAGCCCAAGAGGACGAGCGAGCCCTACGGGCGGCTTACGGAGGCT	7008	
Db	6961	ATCTGTGAAAGCGCGG	GGAGCCCAAGAGGACGAGCGAGCCCTACGGGCGGCTTACGGAGGCT	7020	
QY	7009	ATGACTAGATACT	GTGCCCCCCTGGGGACCCGCCCAACAGAA	TACGACTTGGAGTTG	7068
Db	7021	ATGACTAGATACT	GTGCCCCCCTGGGGACCCGCCCAACAGAA	TACGACTTGGAGTTG	7080
QY	7069	ATAACATCATGCT	CTCCCAATGTGTCAGTTCGCGCAGATGCTGCGAAAAAGGGTGTA	7128	
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QY	7129	TATCTCACCCGCTGAC	CCACCCCTTGGCGGGCTGCGTGGGAGACGCTAGACAC	7188	
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QY	7309	CTAGATTGT	CAGATCTACGGGGCTGTACTCCATGAGCCACTTGACCTACCTCAGATC	7368	
Db	7321	CTAGATTGT	CAGATCTACGGGGCTGTACTCCATGAGCCACTTGACCTACCTCAGATC	7380	
QY	7369	ATTCAAGACT	CCATGGCCTTAGCCATTTCACTCCATAGTTACTCTCCAGGTGAGATC	7428	
Db	7381	ATTCAAGACT	CCATGGCCTTAGCCATTTCACTCCATAGTTACTCTCCAGGTGAGATC	7440	
QY	7429	AATAGGTTGGCT	TCATGCCCTCAGGAACCTTGGGGTACCGCCTTGCAGTCTCGAGGACAT	7488	
Db	7441	AATAGGTTGGCT	TCATGCCCTCAGGAACCTTGGGGTACCGCCTTGCAGTCTCGAGGACAT	7500	
QY	7489	CGGGCCAGAAGT	GTCCGCGCTAGGCTACTGTGCCAGGGGGGAGGGCTGCCACTTGTGGC	7548	
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QY	7549	AAGTACTCT	CTTCAATGCGGACGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCG	7608	
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QY	7609	TCCAGTTCGAT	TATATCCAGCTGGTTTGTGTTGAGCGGGGAGACATATAC	7668	
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QY	7669	AGCCTGTCT	CGTGGCCGACCCCGCTGTTTCATGTGGTGCCTACTCTTCTGTAGGG	7728	
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QY	7729	GTAGGATCTACTACTCCCAACCGATGAACGGGAGCTAAACACATCCAGGCCAAATAGG	7780
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QY	7789	CCATCCTGTTTTTTTCCCTTTTTTTTCTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTT	7848
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QY	7849	TTTTCTCCTTTTTTTTTTCCCTTTTTTTTCTTTTTTTTCTTTTTTTTCTTTTTTTTCTTTT	7908
Db	7861	TTTTCTCCTTTTTTTTTTCCCTTTTTTTTCTTTTTTTTCTTTTTTTTCTTTTTTTTCTTTT	7920
QY	7909	CCTAGTCACGGCTAGCTGTGAAGGTCGTGAGCGGCTTCGACTGCAGAGAGTCTGTATAC	7968
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KEYWORDS			
SOURCE Unknown.			
ORGANISM Unknown.			
REFERENCE			
1 (bases 1 to 8001)			
AUTHORS Bartenschlager,R.			
TITLE Hepatitis C virus culture system			
JOURNAL Patent: US 6630343-A 28 07-OCT-2003;			
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Best Local Similarity 99.7%; Pred. No. 0;			
Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;			
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Db	1	GCAGCCCCCGATTGGGGCGGACATCCACCATAGATCACTCCCTCTGTGAGGAATCTACTG	60
QY	61	TCCTTCACGAGAAAGCGTCTAGCCATGGGTTAGTATGAGTGTGTCGAGCCTCGAGAC	120
Db	61	TCCTTCACGAGAAAGCGTCTAGCCATGGGTTAGTATGAGTGTGTCGAGCCTCGAGAC	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTGCCAG	180
Db	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAAACCGGTGAGTACACCGGAATTGCCAG	180
QY	181	GAGACCGGTCCTTTCTTGGATCAACCGCTCAATGCTGGAGATTGGCGCTGCCCCC	240
Db	181	GAGACCGGTCCTTTCTTGGATCAACCGCTCAATGCTGGAGATTGGCGCTGCCCCC	240
QY	241	GCGAGACTCTAGCCGAGTAGTGTGGTTCGCGAAAGCCCTTTGGTACTCTGTATAGG	300
Db	241	GCGAGACTCTAGCCGAGTAGTGTGGTTCGCGAAAGCCCTTTGGTACTCTGTATAGG	300
QY	301	GTGCTTGGAGTGTCCCGGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCCTAAAC	360
Db	301	GTGCTTGGAGTGTCCCGGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCCTAAAC	360
QY	361	CTCAAGAAACCAACCAAA-----GGCGCGCCATGATTGTAACAAGATGGATTGC	408
Db	361	CTCAAGAAACCAACCAACCAAA-----GGCGCGCCATGATTGTAACAAGATGGATTGC	420

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 469 QY CAATCGGCTGCTCATGCGCGCGGTTCGGCTGTCTAGCGCAGGCGGCGCCGGTTCCTT 528
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 1969 QY TATCATGTGTCGGCTCAAAAGACCTTTGCGGCGCCAAAGGGCCCAATCACCAAAATGATC 2028
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 2209 QY AAGGGCTTTTCGGGCGGTCCACTGCTGCGCCCTCGGCGACGCTGTGGGATCTTTGCG 2268
 2221 DB AAGGGCTTTTCGGGCGGTCCACTGCTGCGCCCTCGGCGACGCTGTGGGATCTTTGCG 2280
 2269 QY GCTCGGCTGTGCAACCCGAGGGGTTGCGAAGCGGTGGAATTTGTACCGGTGAGTCTATG 2328
 2281 DB GCTCGGCTGTGCAACCCGAGGGGTTGCGAAGCGGTGGAATTTGTACCGGTGAGTCTATG 2340
 2329 QY GAAACCACTATGCGGTTCGCGTCTTACGACAACTGCTCCCTCCGCGCTACCGAG 2388
 2341 DB GAAACCACTATGCGGTTCGCGTCTTACGACAACTGCTCCCTCCGCGCTACCGAG 2400
 2389 QY ACATTCAGGTGGCCCATCTACGCGCCCTACTGTTAGCGGCAAGAGCACTAAGGTGCG 2448
 2401 DB ACATTCAGGTGGCCCATCTACGCGCCCTACTGTTAGCGGCAAGAGCACTAAGGTGCG 2460
 2449 QY GCTCGGTATGAGCGCCAAAGGTTAAGGTGTTGTTGAAACCCCTCGTCCGCGCCACC 2508
 2461 DB GCTCGGTATGAGCGCCAAAGGTTAAGGTGTTGTTGAAACCCCTCGTCCGCGCCACC 2520
 2509 QY CTAGGTTTCGGGCGGTATATGTTAAGGCAATGTTATCGACCTTAAACAGAGCCGG 2568
 2521 DB CTAGGTTTCGGGCGGTATATGTTAAGGCAATGTTATCGACCTTAAACAGAGCCGG 2580
 2569 QY GTAAGGACCATCACCGGTCGCCCTACGCTACTCCACCTATGGCAAGTTTCTTGGC 2628

2581 GTAAAGACCATCACACGGGTGCCCCCATCAGTACTCCACCTATGGCAAGTTTCTTGCC 2640
2629 GACGGTGTGTCTGTGGGGGCGCTAATGACATCATATAATATGATGAGTGCCACTCAACT 2688
2641 GACGGTGTGTCTGTGGGGGCGCTAATGACATCATATAATGATGAGTGCCACTCAACT 2700
2689 GACTCGACCACTATCTGTGGGATCGGCACAGTCTCTGGACCAAGCGGAGACGGTGGAGCG 2748
2701 GACTCGACCACTATCTGTGGGATCGGCACAGTCTCTGGACCAAGCGGAGACGGTGGAGCG 2760
2749 CGACTCGTGTGTCTGCCACCGCTACGCTCCGGGATCGGTCCAGCTGCGCATCCAAAC 2808
2761 CGACTCGTGTGTCTGCCACCGCTACGCTCCGGGATCGGTCCAGCTGCGCATCCAAAC 2820
2809 ATCGAGAGGTGGTCTGTCCAGACTGGAGAAATCCCTTTATGGCAAGCCATCCCC 2868
2821 ATCGAGAGGTGGTCTGTCCAGCACTGGAGAAATCCCTTTATGGCAAGCCATCCCC 2880
2869 ATCGAGACCATCAAGGGGGGAGGCACCTCATTTTCTGCGCATCCAAAGAAATGTGAT 2928
2881 ATCGAGACCATCAAGGGGGGAGGCACCTCATTTTCTGCGCATCCAAAGAAATGTGAT 2940
2929 GAGTCCGCGGAAAGCTGTCCGGGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTT 2988
2941 GAGTCCGCGGAAAGCTGTCCGGGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTT 3000
2989 GATGTATCCGTCATACCAACTAGGGGAGAGCTGATTTGTGTAGCAACGAGCTCTAATG 3048
3001 GATGTATCCGTCATACCAACTAGGGGAGAGCTGATTTGTGTAGCAACGAGCTCTAATG 3060
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3109 GTGACTTACGCTTGACCCGACCTTACCAATGAGACGACGACGCTGCTGCAATGATGTGTACCCAGACA 3168
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3169 GTGTACGCTTGACCCGACGAGGAGGAGCTGTTAGGGGAGGATGGGCAATTTACAGGTTT 3228
3181 GTGTACGCTTGACCCGACGAGGAGGAGCTGTTAGGGGAGGATGGGCAATTTACAGGTTT 3240
3229 GTGACTTACGAGAAACGGCTCGGGCATGTTCAATTCCTCGGTTCTGTGCGAGTGTAT 3288
3241 GTGACTTACGAGAAACGGCTCGGGCATGTTCAATTCCTCGGTTCTGTGCGAGTGTAT 3300
3289 GACCGGGCTGTGTTGTGTACGAGCTCACGCGCCCGCAGACCTCAGTTAGTGTTCGGGCT 3348
3301 GACCGGGCTGTGTTGTGTACGAGCTCACGCGCCCGCAGACCTCAGTTAGTGTTCGGGCT 3360
3349 TACTTAAACACACAGGTTTGGCGTCTGCGAGACCATCTGGAGTTCTGGGAGAGCGTC 3408
3361 TACTTAAACACACAGGTTTGGCGTCTGCGAGACCATCTGGAGTTCTGGGAGAGCGTC 3420
3409 TTTTACAGGCTTACCCACATAGAGCGCCATTTCTGTGTCAGACTAAGCGAGGAGGAGAC 3468
3421 TTTTACAGGCTTACCCACATAGAGCGCCATTTCTGTGTCAGACTAAGCGAGGAGGAGAC 3480
3469 AACTTCCCTTACCTGTGTAGCATACCAAGGCTACGTTGTGCGCCAGGCTCAGGCTCCACCT 3528
3481 AACTTCCCTTACCTGTGTAGCATACCAAGGCTACGTTGTGCGCCAGGCTCAGGCTCCACCT 3540
3529 CCATCGTGGACCAATGTGGAAGTGTCTCATACGCTTAAAGCTTACGCTGCAACCGGCCA 3588
3541 CCATCGTGGACCAATGTGGAAGTGTCTCATACGCTTAAAGCTTACGCTGCAACCGGCCA 3600
3589 ACGCCCTTCTGTATAGGCTGGAGCGGTTCAAAACAGGTTACTACCAACACCCCATTA 3648
3601 ACGCCCTTCTGTATAGGCTGGAGCGGTTCAAAACAGGTTACTACCAACACCCCATTA 3660
3649 ACCAAATACATCATGCGATGCGTGTGCGTGTGAGGCTGTGCGAGGCTGTGCGGCGG 3708
3661 ACCAAATACATCATGCGATGCGTGTGCGTGTGAGGCTGTGCGAGGCTGTGCGGCGG 3720

3709 CTGCTAGCGGAGTCTCTAGACGCTCTGGCGCGGTATTTGCTGACAAACAGCAGCGTGGTC 3768
3721 CTGCTAGCGGAGTCTCTAGACGCTCTGGCGCGGTATTTGCTGACAAACAGCAGCGTGGTC 3780
3769 ATTGTGGGCGAGGATCATCTTTGTCCGAAAGCCGCGCATCATTTCCCGACAGGGAAGTCTTT 3828
3781 ATTGTGGGCGAGGATCATCTTTGTCCGAAAGCCGCGCATCATTTCCCGACAGGGAAGTCTTT 3840
3829 TACCGGAGTTCGATGAGATGGAAGTGGCTCACACCTCCCTTACATCGAAACAGGCA 3888
3841 TACCGGAGTTCGATGAGATGGAAGTGGCTCACACCTCCCTTACATCGAAACAGGCA 3900
3889 ATGCAAGCTCGCGCAACATTTCAAACAGAGGCAATTCGGGTCTGCTGCAACAGCCCAAG 3948
3901 ATGCAAGCTCGCGCAACATTTCAAACAGAGGCAATTCGGGTCTGCTGCAACAGCCCAAG 3960
3949 CAAGCGAGGCTGTCTCTCCGTTGGTGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGG 4008
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4021 GCGAAGCATATGTGGAATTTTCATCAGCGGATACAATATTTAGCAGGCTTGTCCACTGTG 4080
4069 CTTGCAACCCCGGATAGCATCTGATGGAATTCACAGCTCTATCACAGCCCGCTC 4128
4081 CTTGCAACCCCGGATAGCATCTGATGGAATTCACAGCTCTATCACAGCCCGCTC 4140
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4141 ACCACCAACATACCTCTCTTTAAACATCTGGGGGATGGTGGCGCCCACTTCT 4200
4189 CTTCCAGCGCTCTCTGCTTTCTAGGCGCCGCGCATCTGCTGAGCGGCTGTTGGCAGC 4248
4201 CTTCCAGCGCTCTCTGCTTTCTAGGCGCCGCGCATCTGCTGAGCGGCTGTTGGCAGC 4260
4249 ATAGGCTTGGGAGGCTGTTGGATATTTTGGCAGGTTATGAGCAGGCTGGCAGGC 4308
4261 ATAGGCTTGGGAGGCTGTTGGATATTTTGGCAGGTTATGAGCAGGCTGGCAGGC 4320
4309 GCGCTCTGCGCTTTAAGGTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAAC 4368
4321 GCGCTCTGCGCTTTAAGGTCATGAGCGGAGTGGCTTCCACCGAGGACCTGGTTAAC 4380
4369 CTAATCCCTCTATPCTCTCCCTTGGCGCCCTAGTCTGCGGGTCTGTCGCGAGCGATA 4428
4381 CTAATCCCTCTATPCTCTCCCTTGGCGCCCTAGTCTGCGGGTCTGTCGCGAGCGATA 4440
4429 CTTGCTGCGGACCTGGGCGCCAGGGAGGGGCTGTGCAATGATGAACCGGCTGATAGCG 4488
4441 CTTGCTGCGGACCTGGGCGCCAGGGAGGGGCTGTGCAATGATGAACCGGCTGATAGCG 4500
4489 TTTGCTTCCGCGGTTAAACACAGCTCTCCCGCAGCTATGCTGCTGAGCAGCGCTGCA 4548
4501 TTTGCTTCCGCGGTTAAACACAGCTCTCCCGCAGCTATGCTGCTGAGCAGCGCTGCA 4560
4549 GCAGGTCACCTCAGATCTCTCTAGTCTTACCATCAGCTCAGCTGCTGAAGAGGCTTAC 4608
4561 GCAGGTCACCTCAGATCTCTCTAGTCTTACCATCAGCTCAGCTGCTGAAGAGGCTTAC 4620
4609 CAGTGGATCAACGAGGACTGTGATGATTTCAAGACTGTGCTGCTGCTAAGAGATGTTGG 4668
4621 CAGTGGATCAACGAGGACTGTGCTCCAGCCTGTCCCGCTGCTGCTAAGAGATGTTGG 4680
4669 GATTGATATGACCGTGTGATGATTTCAAGACTGTGCTGCTGCTAAGAGATGTTGG 4728
4681 GATTGATATGACCGTGTGATGATTTCAAGACTGTGCTGCTGCTAAGAGATGTTGG 4740
4729 CGATTCCGCGGAGTCCCTTCTCTTCTCATGTCAACGTGGGTACAGGAGCTGTGGCGGGC 4788
4741 CGATTCCGCGGAGTCCCTTCTCTTCTCATGTCAACGTGGGTACAGGAGCTGTGGCGGGC 4800

QY	4789	GACGGCATCATGCAAAACCACTTGCCCAATGTGAGACACAGATCACCCGGACATGTGAAAAC	4848
DB	4801	GACGGCATCATGCAAAACCACTTGCCCAATGTGAGACACAGATCACCCGGACATGTGAAAAC	4860
QY	4849	GGTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACATTCCCC	4908
DB	4861	GGTTCCATGAGGATCGTGGGGCTTAGGACCTGTAGTAACACGTGGCATGGAACATTCCCC	4920
QY	4909	ATTAACGGCTACACACACGGGCCCTCTCAGCCCTCCCGCGGCCAAATATTCTAGGGCG	4968
DB	4921	ATTAACGGCTACACACACGGGCCCTCTCAGCCCTCCCGCGGCCAAATATTCTAGGGCG	4980
QY	4969	CTGTGCGGGTGGCTGCTCAGGAGTAGTGGAGGTTACGCGGTTGGGGATTTCCACTAC	5028
DB	4981	CTGTGCGGGTAGTGTCTGAGGAGTAGTGGAGGTTACGCGGTTGGGGATTTCCACTAC	5040
QY	5029	GTGACGGGCATGACCACTGACAACTGAAGTGCCCGTGTGAGTTCCGGCGCCCGAATTC	5088
DB	5041	GTGACGGGCATGACCACTGACAACTGAAGTGCCCGTGTGAGTTCCGGCGCCCGAATTC	5100
QY	5089	TTTACAGAACTGATGGGTGCGGTGTCACAGGTACGCTCCAGCGTGCAAAACCCCTCCTA	5148
DB	5101	TTTACAGAACTGATGGGTGCGGTGTCACAGGTACGCTCCAGCGTGCAAAACCCCTCCTA	5160
QY	5149	CGGAGGAGTGCATTTCTCGTTCGGGCTCAATCAATACCTTGGTTCACAGCTCCCA	5208
DB	5161	CGGAGGAGTGCATTTCTCGTTCGGGCTCAATCAATACCTTGGTTCACAGCTCCCA	5220
QY	5209	TGGAGCCGAAACCGGACGTAGCAGTGTCTACTTCCATGTCTACGACCCCTCCACATT	5268
DB	5221	TGGAGCCCTGAACCGGATGTAGCAGTGTCTACTTCCATGTCTACGACCCCTCCACATT	5280
QY	5269	ACGGCGAGACCGCTAAGCGTAGCGTGGCCAGGGGATCTCCGCCCTCTTGGCCAGCTCA	5328
DB	5281	ACGGCGAGACCGCTAAGCGTAGCGTGGCCAGGGGATCTCCGCCCTCTTGGCCAGCTCA	5340
QY	5329	TCAGTACCGACGTGTCTGCGCCTTCTCTTGAAGGCAACATGCACTACCCGTCATGACTCC	5388
DB	5341	TCAGTACCGACGTGTCTGCGCCTTCTCTTGAAGGCAACATGCACTACCCGTCATGACTCC	5400
QY	5389	CCGACGCTGACCTCATCAGGCCAACCTCTGTGGCGGAGAGATGGCGGGGAACATC	5448
DB	5401	CCGACGCTGACCTCATCAGGCCAACCTCTGTGGCGGAGAGATGGCGGGGAACATC	5460
QY	5449	ACCCCGTGGAGTCAAAAAATAGGTAGTAATTTTGGACTCTTTTCGAGCCGCTCCAAGCG	5508
DB	5461	ACCCCGTGGAGTCAAAAAATAGGTAGTAATTTTGGACTCTTTTCGAGCCGCTCCAAGCG	5520
QY	5509	GAGGAGGATGAGAGGAGATTCCTGTCGGCGGAGATCTCTGGAGGTCCTCAGGAAATTC	5568
DB	5521	GAGGAGGATGAGAGGAGATTCCTGTCGGCGGAGATCTCTGGAGGTCCTCAGGAAATTC	5580
QY	5569	CCTCAGCGATGCCATATGGGACGCGCCGGATTAACCCCTCCACTGTTAGAGTCTCTGG	5628
DB	5581	CCTCAGCGATGCCCNATATGGGACGCGCCGGATTAACCCCTCCACTGTTAGAGTCTCTGG	5640
QY	5629	AAGGACCCGACTACGTCCCTCAGTGTGTACCGGGTGTCCATTCGCCGCTGCCAAGGCC	5688
DB	5641	AAGGACCCGACTACGTCCCTCAGTGTGTACCGGGTGTCCATTCGCCGCTGCCAAGGCC	5700
QY	5689	CCTCCGATACCACTTCCAGGAGGAGAGAGAGTGTCTGTGCAAACTCTACCGTGTCT	5748
DB	5701	CCTCCGATACCACTTCCAGGAGGAGAGAGAGTGTCTGTGCAAACTCTACCGTGTCT	5760
QY	5749	CTGTCTTGGCGAGTCTGCGCAAAAAGACCTTCGGCAGCTCCGAATCGTCGGCGCTCGAC	5808
DB	5761	CTGTCTTGGCGAGTCTGCGCAAGAGACCTTCGGCAGCTCCGAATCGTCGGCGCTCGAC	5820
QY	5809	AGCGGCACGCCAACCGGCTCTCTGACCGACCCCTCCGACGCGGAGCGGGATCCGAC	5868
DB	5821	AGCGGCACGCCAACCGGCTCTCTGACCGACCCCTCCGACGCGGAGCGGGATCCGAC	5880
QY	5869	GTTGAGTGTACTCTCTCCATGCCCCCTTTGAGGGGAGCGGGGGATCCCGATCTCAGC	5928

5881 GTTGA GTCTACTCTCTCCATGCCCCCTTGAGGGGGAGCCGGGGATCCCGATCTCAGC 5940

5929 GACGGCTTTGGTCTACCGTAAGCAGGAGGCTACTGAGGACGTCGTCGTCTGCTCGATG 5988

5941 GACGGCTTTGGTCTACCGTAAGCAGGAGGCTACTGAGGACGTCGTCGTCTGCTCGATG 6000

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6121 CGAGCGCAAACTCGGCGAAGAGGTCACCTTTGACAGACTCGCGTCTCTGGACGAC 6180

6169 CACTACCGGACCTGTCTAAGAGATGAAGGGCAAGGCGTCCACAGTTAAGGCTAAACTTT 6228

6181 CACTACCGGACCTGTCTAAGAGATGAAGGGCAAGGCGTCCACAGTTAAGGCTAAACTTT 6240

6229 CTATCCGTGGAGGAAGCTCTAAGCTGA CGCCGCCACATTCGGCAGATCTAAATTTGGC 6288

6241 CTATCCGTGGAGGAAGCTCTAAGCTGA CGCCGCCACATTCGGCAGATCTAAATTTGGC 6300

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6301 TATGGGGCAAGGAGCTCCGGAACCTATCAGCAAGCGCGTTAAACCACATCCGCTCCGCTG 6360

6349 TGGAGGACTTGTGGGAAGCACTGACACACCAATTTGACACCACTATGSCAAAAAT 6408

6361 TGGAGGACTTGTGGGAAGCACTGACACACCAATTTGACACCACTATGSCAAAAAT 6420

6409 GAGGTTTTCTCGTCCAAACAGAGAAAGGGGGCGGACGAGCTCGCTTATCGTTATTC 6468

6421 GAGGTTTTCTCGTCCAAACAGAGAAAGGGGGCGGACGAGCTCGCTTATCGTTATTC 6480

6469 CCAGATTTGGGGTTCTGTGTGCGGAAATGSCCCTTTACGATGTGGTCTCCACCCCTC 6528

6481 CCAGATTTGGGGTTCTGTGTGCGGAAATGSCCCTTTACGATGTGGTCTCCACCCCTC 6540

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6541 CCTCAGGCGGTGATGGGCTCTTCATACGGATTCCAATACTCTCTCGACAGCGGTCGAG 6600

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6649 TGTTTTGACTCAACGGTCACTGAGATGACATCCGTTGAGGAGTCAATCTACCAATGT 6708

6661 TGTTTTGACTCAACGGTCACTGAGATGACATCCGTTGAGGAGTCAATCTACCAATGT 6720

6709 TGTGACTTGGCCCCCGAAGCCAGACAGGCCATAGGTCGCTCACAGAGCGCTTTACATC 6768

6721 TGTGACTTGGCCCCCGAAGCCAGACAGGCCATAGGTCGCTCACAGAGCGCTTTACATC 6780

6769 GGGGGCCCCCTGACTAATTTCTAAGGGCAGAACTCGCGCTATCGCGTGGCGGCGAGC 6828

6781 GGGGGCCCCCTGACTAATTTCTAAGGGCAGAACTCGCGCTATCGCGTGGCGGCGAGC 6840

6829 GGTGTACTGACGACGCTGCGGTAACTCCCTCACATGTTACTTTGAAGCGCGTCCGCGC 6888

6841 GGTGTACTGACGACGCTGCGGTAACTCCCTCACATGTTACTTTGAAGCGCGTCCGCGC 6900

6889 TGTGAGCTCGGAAGCTCCAGGACTGCAAGTCTCGTATCGGAGACGACTTGTGCTTT 6948

6901 TGTGAGCTCGGAAGCTCCAGGACTGCAAGTCTCGTATCGGAGACGACTTGTGCTTT 6960

6949 ATCTGTGAAGCGCGGGACCCCAAGAGGACGAGGCGCTTACGGGCTTCCAGGAGCT 7008

RESULT 13
AX036261

QY	709	CTCTGCGGAGAAAGTATCCATCATGGCTGATGCAATCGGCGGTGTCATCGCTTGATC	768	Db	1801	CACGATAATACCATGGCGCCTATTACGGCCTACTCCCAACAGACCGGAGGCTACTTTGGC	1860
Db	721	CTCTGCGGAGAAAGTATCCATCATGGCTGATGCAATCGGCGGTGTCATCGCTTGATC	780	QY	1849	TGCATCATCACTAGCTCACAAGCGGACAGAGAAACAGAGGTGAGGGGAGGTCCAAAGTG	1908
QY	769	CGGCTACCTGCGCCATTGACACCAAGCAAGCAACATCGCATCGAGCGAGCACCTACTCGGA	828	Db	1861	TGCATCATCACTAGCTCACAAGCGGACAGAGAAACAGAGGTGAGGGGAGGTCCAAAGTG	1920
Db	781	CGGCTACCTGCGCCATTGACACCAAGCAACATCGCATCGAGCGAGCACCTACTCGGA	840	QY	1909	GTCTCCACCGCAACAATCTTTCTCTGGCGACCTCGCTCAATGCGGTCAATGCGGTGTTGGATGTC	1968
QY	829	TGGAAGCGGCTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAG	888	Db	1921	GTCTCCACCGCAACAATCTTTCTCTGGCGACCTCGCTCAATGCGGTGTTGGATGTC	1980
Db	841	TGGAAGCGGCTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAG	900	QY	1969	TATCATGTTGCGGCTCAAAAGACCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTAC	2028
QY	889	CGGAATGTTGCGGAGGTCAAGGCGCGCATGCGCGACGCGAGGATCTCGTCTGACCC	948	Db	1981	TATCATGTTGCGGCTCAAAAGACCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTAC	2040
Db	901	CGGAATGTTGCGGAGGTCAAGGCGCGCATGCGCGACGCGAGGATCTCGTCTGACCC	960	QY	2029	ACCAATGTGGACAGGACCTCGTCTGGTGGCAAGGCGCCCGGGGCGGTTCTTGTACA	2088
QY	949	ATGGGATGCTCTGTCGCGCATATCATGTTGGAATGCGCGCTTTCTGGATTCAATCG	1008	Db	2041	ACCAATGTGGACAGGACCTCGTCTGGTGGCAAGGCGCCCGGGGCGGTTCTTGTACA	2100
Db	961	ATGGGATGCTCTGTCGCGCATATCATGTTGGAATGCGCGCTTTCTGGATTCAATCG	1020	QY	2089	CCATGCACCTGCGGAGCTCGGACCTTTACTTGGTCAAGGACATGCGGATGTCATTCG	2148
QY	1009	ACTGTGCGCGGCTGGGTGTGGCGACCGGTATCAGGACATAGGTTGGCTACCCGTGATA	1068	Db	2101	CCATGCACCTGCGGAGCTCGGACCTTTACTTGGTCAAGGACATGCGGATGTCATTCG	2160
Db	1021	ACTGTGCGCGGCTGGGTGTGGCGACCGGTATCAGGACATAGGTTGGCTACCCGTGATA	1080	QY	2149	GTGCGCGGCGGCGGACAGAGGGGAGGCTACTCTCCCGGAGGCGGCTCTCTACTTG	2208
QY	1069	TTGCTGAAGAGCTTGGCGGGAATGGCTGACCGCTTCCTCGTCTTACGTTACGGTATCGCG	1128	Db	2161	GTGCGCGGCGGCGGACAGAGGGGAGGCTACTCTCCCGGAGGCGGCTCTCTACTTG	2220
Db	1081	TTGCTGAAGAGCTTGGCGGGAATGGCTGACCGCTTCCTCGTCTTACGTTACGGTATCGCG	1140	QY	2209	AGGGGCTCTTGGCGGCTCGACCTCTGCTCTCGGCGGACGCTCTCGGCGGCGGCTCTTTCGG	2268
QY	1129	CTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAA	1188	Db	2221	AGGGGCTCTTGGCGGCTCGACCTCTGCTCTCGGCGGACGCTCTCGGCGGCGGCTCTTTCGG	2280
Db	1141	CTCCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAA	1200	QY	2269	GCTGCGGTGTGACCCGAGGGGTTGCAAGGCGGTGCACTTTGTATCCGTCGAGTCTATG	2328
QY	1189	CAGACACAAACGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTGCTCCCGCCCGCT	1248	Db	2281	GCTGCGGTGTGACCCGAGGGTTCGCAAGGCGGTGCACTTTGTATCCGTCGAGTCTATG	2340
Db	1201	CAGACACAAACGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTGCTCCCGCCCGCT	1260	QY	2329	GAAACACATATGCGGTCCCGGCTTTCACGAGCACTCGTCCCTCGCGCGCTACCGCAG	2388
QY	1249	AAGTTACTGCGGAGCGCTTGGATTAAGCGGTGCGGTTGCTATATGTTATTT	1308	Db	2341	GGAACACATATGCGGTCCCGGCTTTCACGAGCACTCGTCCCTCGCGCGCTACCGCAG	2400
Db	1261	AAGTTACTGCGGAGCGCTTGGATTAAGCGGTGCGGTTGCTATATGTTATTT	1320	QY	2389	ACATTCAGGTGCGCCATCTACACGCGCTTACTGGTAGCGGCAAGAGCACTTAAGGTGCG	2448
QY	1309	TCACCATATGCGGCTCTTTGGCAATGTAGGCGCCCGGAAACCTGCGCCCTGCTCTTG	1368	Db	2401	ACATTCAGGTGCGCCATCTACACGCGCTTACTGGTAGCGGCAAGAGCACTTAAGGTGCG	2460
Db	1321	TCACCATATGCGGCTCTTTGGCAATGTAGGCGCCCGGAAACCTGCGCCCTGCTCTTG	1380	QY	2449	GCTGCGTATGACGCCAAGGGTATAGGTGTTGCTCTGAACCCGTCGTCGCGCGCCACC	2508
QY	1369	ACGAGCATTCCTAGGGTCTTCCCTCTGCGCAAGAGATGCAAGTCTGTTGAATGTC	1428	Db	2461	GCTGCGTATGACGCCAAGGGTATAGGTGTTGCTCTGAACCCGTCGTCGCGCGCCACC	2520
Db	1381	ACGAGCATTCCTAGGGTCTTCCCTCTGCGCAAGAGATGCAAGTCTGTTGAATGTC	1440	QY	2509	CTAGGTTTCGGGGGTATATGTTCTAAGGCACATGCTACGACCTTAACATCAGAACCGGG	2568
QY	1429	GTGAAGGACAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACTGTTAGCGACCCCTT	1488	Db	2521	CTAGGTTTCGGGGGTATATGTTCTAAGGCACATGCTACGACCTTAACATCAGAACCGGG	2580
Db	1441	GTGAAGGACAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACTGTTAGCGACCCCTT	1500	QY	2569	GTAAGGACCATCACCGGTCGCCCATCACGTAATCTCCACCTATGGCAAGTTCCTTGCC	2628
QY	1489	TGCAGGACAGCGAACCCTCCCTGGGACAGGTGCTCTCGGCGCAAAAGCCACGTGTA	1548	Db	2581	GTAAGGACCATCACCGGTCGCCCATCACGTAATCTCCACCTATGGCAAGTTCCTTGCC	2640
Db	1501	TGCAGGACAGCGAACCCTCCCTGGGACAGGTGCTCTCGGCGCAAAAGCCACGTGTA	1560	QY	2629	GACGCGTGTGCTCTGCGGGCGCTATGACATCATATATATGATGAGTGCACCTCAACT	2688
QY	1549	TAAGATACACTGAAAGGCGGCAACCCAGTGCACAGTGTGAGTTGATGTTG	1608	Db	2641	GACGCGTGTGCTCTGCGGGCGCTATGACATCATATATATGATGAGTGCACCTCAACT	2700
Db	1561	TAAGATACACTGAAAGGCGGCAACCCAGTGCACAGTGTGAGTTGATGTTG	1620	QY	2689	GACTCGACCATATCTCTGGGATCGGCACAGTCTCTGGACCAAGCGGAGACGCGTGGAGCG	2748
QY	1609	GAAAGTCAATGCTCTCTCAAGCTTATCAAGAGGCTTGAAGAGTGCAGGAGGCGG	1668	Db	2701	GACTCGACCATATCTCTGGGATCGGCACAGTCTCTGGACCAAGCGGAGACGCGTGGAGCG	2760
Db	1621	GAAAGTCAATGCTCTCTCAAGCTTATCAAGAGGCTTGAAGAGTGCAGGAGGCGG	1680	QY	2749	CGACTCGTGTGCTCGCCACCGCTACGCTCTCGGGATCGGTACCGTGCACATCCAAAC	2808
QY	1669	GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACATGTTTACATGTTTATG	1728	Db	2761	CGACTCGTGTGCTCGCCACCGCTACGCTCTCGGGATCGGTACCGTGCACATCCAAAC	2820
Db	1681	GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACATGTTTACATGTTTATG	1740	QY	2809	ATCGAGGAGGTGCTCTCTCGAGCACTGGAGAAATCCCTTTTATGGCAAGGAGGAGTCC	2868
QY	1729	TCGAGGTTAAAAAGCTCTAGGCCCCCGAACAAGGAGGCTGTTTCTTCTTCAAAA	1788	Db	2821	ATCGAGGAGGTGCTCTCTCGAGCACTGGAGAAATCCCTTTTATGGCAAGGAGGAGTCC	2880
Db	1741	TCGAGGTTAAAAAGCTCTAGGCCCCCGAACAAGGAGGCTGTTTCTTCTTCAAAA	1800	QY	2869	ATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2928
QY	1789	CACGATAATACCATGGCGCTATTACGGCCTACTCCCAACAGACGCGGCGCTACTTGGC	1848				

Db 2881 ATCGAGACCATCAAGGGGGGAGCGACCTCATTTTCTGCCAATTCGAAGAAGAAATGTGAT 2940
QY 2929 GAGCTCGCGCGAAGCTGTCCGCTCGGACTCAATGCTGTAGCAATATTACCGGGGCTT 2988
Db 2941 GAGCTCGCGCGAAGCTGTCCGCTCGGACTCAATGCTGTAGCAATATTACCGGGGCTT 3000
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QY 3229 GTGACTTCAGGAGAAACGGCCCTCGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTCTAT 3288
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Db 3721 CTGGTAGGCGGAGTCTTAGCAGCTCTGGCGGCTATTGCTGACAAAGCAGGAGGCTG 3780
QY 3769 ATTGTGGGAGGATCATCTTTGTCCGAAAGCGGCGCATATTCCCGACAGGAGTCTT 3828
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Db	5101	TTCAAGAGTGGATGGGTGGGTTGACAGGTACGCTCCAGCGGTGAAACCCCTCCTA	5160	QY	6229	CTATCCGTGGAGAAAGCTGTAAAGCTGACGCCCCACATTTGGCCAGATCTMAATTTGGC	6288
QY	5149	CGGAGGAGGTACATTTCTGTGTGGGTCAATCAATACCTGTGGTTCACAGCTCCCA	5208	Db	6241	CTATCCGTGGAGAAAGCTGTAAAGCTGACGCCCCACATTTGGCCAGATCTMAATTTGGC	6300
Db	5161	CGGAGGAGGTACATTTCTGTGTGGGTCAATCAATACCTGTGGTTCACAGCTCCCA	5220	QY	6289	TATGGGGCAAGGACGTCCGGAACCTATCCAGAAAGCGGTTAAACACATCCGCTCCGTG	6348
QY	5209	TGCGAGCCGAAACCGGACGTAGCAGTGTCTCATTCATGCTCACGACCCCTCCCACT	5268	Db	6301	TATGGGGCAAGGACGTCCGGAACCTATCCAGAAAGCGGTTAAACACATCCGCTCCGTG	6360
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QY	5269	ACGGCGGACGCTAAGCGTAGGCTGGCCAGGGATCTCCCTCTCTTGGCCAGCTCA	5328	Db	6361	TGGAAGGACTTCTGTGAAGACACTGAGACACCAATTTGACACCACTCATGCAAAAT	6420
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QY	5329	TGAGCTAGCAGCTGTCTGGCTTCTTGAAGGCAACATGCACTACCGTCTATGACTCC	5388	Db	6421	GAGGTTTTCTGTGTCCAAACAGAGAGGGGGCGCAAGCGAGCTCGCTTATCGTATTC	6480
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QY	5749	TCTGCTTGGCGAGCTGCCAAGAACCTTGGCAGCTCCGATCTGCGCGCTGAC	5808	Db	6841	GGTGTACTGACGAGCTGCGGTAAATACCTTCATGTTTGAAGCGGCTTGCAGCC	6900
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QY	5809	AGCGGACGCAACGCGCTCTCTGACAGCCCTCCGACGAGCGGCGGAGATCCGAC	5868	Db	6901	TGTGAGCTGGAAGCTCCAGACTGACAGGTCTGCTGCTATGCGGAGACGACTTGTCTGT	6960
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QY	5869	GTGAGTGTACTCTCTCCATGCCCCCTTGAAGGAGGAGCGGCGGATCCGATCTGAC	5928	Db	6961	ATCTGTGAAAGCGGGGACCCAAAGAGGACGAGGCGAGCTTACGGGCTTACCGAGGCT	7020
Db	5881	GTGAGTGTACTCTCTCCATGCCCCCTTGAAGGAGGAGCGGCGGATCCGATCTGAC	5940	QY	7009	ATGACTAGTACTCTGCCCCCTTGGGACCCGCCCAACCAAGATACGACTTGGAGTTG	7068
QY	5929	GACGGTCTTGTCTACCGTAGCAGGAGCTAGTAGGAGCTGCTGTGCTGCTGATG	5988	Db	7021	ATGACTAGTACTCTGCCCCCTTGGGACCCGCCCAACCAAGATACGACTTGGAGTTG	7080
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QY	6169	CACTACCGGACGCTGCTCAAGGAGATGAAGGCGAAGGCGTCCACAGTTAAGGTAAACTT	6228				

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QY	5958	GGCTAGTGAGACGCTCTGCTGCTCGATGCTCTACACATGGACAGCGGCCCTGATCAC	6017	7038	CCGCCCCAACCAAGATACGACTTGGAGTTGATAACATCATGCTCTCTCAATGTGTGAGT
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QY	6018	GCCATGCGCTCGGAGGAACCAAGCTGCCCATCAATGCACTGAGCACTCTTTGCTCCG	6077	7098	CGCGCAGCATGCTTGGCAAAAGGGTGTACTATCTCACCGGTGACCCACACCCCCCT
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QY	6438	GGGCGGAGCGCTGCTGCTATGCTATCCAGATTTGGGGTTCGTTGTCGAGAA	6497	7578	CAAGCTCAAACTCACTCCAAATCCCGCTCGGTCCAGTTGGATTTATCCAGCTGGTCTGT
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QY	6558	ATTCCAAATCTCTCTGGACAGCGGGTTCGATGCTGCTGGAATGCTGGAAGCGAAGAA	6617	7757	CATGCTGGTCTACTCTCTACTTCTGTAGGGGTAGGCATCTATCTACTCCCCAACCGATG
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QY	6678	CATCGGTTGAGGAGTCAATCTACCAATGTGTGACTTGGCCCCCGAAGCCAGACGCG	6737	8809	AACGGGAGCTTAAACACTTCCAGGCCAATAGGCCAATCTGTTTTTCTTTTTTTTTTTT
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ACCESSION AX937621
VERSION AX937621.1 GI:40713672
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SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
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AUTHORS Duggal,R.A., Patrick,A.K., Zhang,J.A. and Zhao,W.A.
TITLE Reporter-selectable hepatitis c virus replicon
JOURNAL Patent: WO 03091439-A 1 06-NOV-2003;
PFIZER INC. (US)
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7989	100.0	7989	4	US-09-539-601-10
2	7967	99.7	8001	4	US-09-539-601-7
3	7949.4	99.5	8001	4	US-09-539-601-22
4	7947.8	99.4	8001	4	US-09-539-601-16
5	7941.4	99.4	8001	4	US-09-539-601-28
6	7331	91.7	8637	4	US-09-539-601-4
7	7309	91.5	8649	4	US-09-539-601-13
8	7273.8	91.0	8639	4	US-10-029-907-1
9	7272.8	91.0	8638	4	US-10-029-907-24
10	7249.8	90.7	8638	4	US-10-029-907-7
11	7248.8	90.7	8638	4	US-10-029-907-25
12	7246.8	90.7	8642	4	US-10-029-907-2
13	7245.6	90.7	8638	4	US-10-029-907-6
14	7229.8	90.5	8648	4	US-10-029-907-5
15	7222.6	90.4	8643	4	US-10-029-907-4
16	6186.8	77.4	11076	4	US-09-539-601-1
17	6169.2	77.2	11076	4	US-09-539-601-25
18	6167.6	77.2	11076	4	US-09-539-601-19
19	6161.2	77.1	11076	4	US-09-539-601-31
20	5318.4	66.5	9595	3	US-09-014-416-4
21	5218	65.3	7917	1	US-08-324-977-31
22	5218	65.3	7917	2	US-08-384-616-31
23	5218	65.3	7917	2	US-08-904-686A-31
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28 5218 65.3 9416 3 US-09-315-850-1 Sequence 1, Appli
29 5218 65.3 9416 4 US-08-823-895A-27 Sequence 27, Appli
30 5211.8 65.2 9472 4 US-08-150-204E-96 Sequence 96, Appli
31 5175.2 64.8 7863 1 US-08-324-977-35 Sequence 35, Appli
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39 4103.8 51.3 9599 3 US-09-014-416-2 Sequence 2, Appli
40 4102.2 51.3 9599 3 US-09-014-416-6 Sequence 6, Appli
41 4097.8 51.3 9646 3 US-08-811-566-1 Sequence 1, Appli
42 4097.8 51.3 9646 3 US-09-034-756-1 Sequence 1, Appli
43 4094.2 51.2 12980 3 US-08-811-566-5 Sequence 5, Appli
44 4094.2 51.2 12980 3 US-09-034-756-5 Sequence 5, Appli
45 4021.4 50.3 9379 3 US-09-388-874-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-539-601-10
; Sequence 10, Application US/09539601C
; Patent No. 8630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I377/NS3-3' /wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1181)
; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase
; OTHER INFORMATION: fusion protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1190)..(1800)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1801)..(7758)
; OTHER INFORMATION: hepatitis C virus NS3 - 5B
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7759)..(7989)
; PUBLICATION INFORMATION:
; AUTHORS: Lohmann, Volker
; AUTHORS: Kner, Frank
; AUTHORS: Koch, Jan-Oliver
; AUTHORS: Herian, Ulrike
; AUTHORS: Theilmann, Lorenz
; AUTHORS: Bartenschlager, Ralf
; TITLE: Replication of subgenomic hepatitis C virus RNAs in a
; JOURNAL: Science
; VOLUME: 285

PAGES: 110-113									
DATE: 1999-07-02									
US-09-539-601-10									
Query Match 100.0%; Score 7989; DB 4; Length 7989;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	TCTTCACGAGAAACGCTCTAGCCATAGCGGTGTAGTATGAGTGTCTGTCAGCTCCAGAC	120						
Db	61	TCTTCACGAGAAACGCTCTAGCCATAGCGGTGTAGTATGAGTGTCTGTCAGCTCCAGAC	120						
QY	121	CCCCCTCCGGGAGAGCATAGTGTCTGCGGAACCGGTAGTACACCGGAATGGCCAG	180						
Db	121	CCCCCTCCGGGAGAGCATAGTGTCTGCGGAACCGGTAGTACACCGGAATGGCCAG	180						
QY	181	GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGCTGCCGCC	240						
Db	181	GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGAGATTTGGGGCTGCCGCC	240						
QY	241	GGGAGCTCTAGCCGAGTGTGTGGGTGCGGAAGGCTTGTGTACTGCTGATAGG	300						
Db	241	GGGAGCTCTAGCCGAGTGTGTGGGTGCGGAAGGCTTGTGTACTGCTGATAGG	300						
QY	301	GTGCTTGGAGTGGCCCGGAGGTCTGCTAGACCGGTGCAACCATGACGAACTCTTAAC	360						
Db	301	GTGCTTGGAGTGGCCCGGAGGTCTGCTAGACCGGTGCAACCATGACGAACTCTTAAC	360						
QY	361	CTCAAGAAAAACAAAGGCGCGCATGATGAAACAAGTGAATGCGAGGTTCTC	420						
Db	361	CTCAAGAAAAACAAAGGCGCGCATGATGAAACAAGTGAATGCGAGGTTCTC	420						
QY	421	CGGCCGCTTGGGTGGAGAGCTATTGGCTATGACTGGGCACACAGACAACTCGGTCT	480						
Db	421	CGGCCGCTTGGGTGGAGAGCTATTGGCTATGACTGGGCACACAGACAACTCGGTCT	480						
QY	481	CTGATGCGCGGTTCCTCGGCTGTACGCGAGGGGCGCGGTTCTTTTGTCAAGACCG	540						
Db	481	CTGATGCGCGGTTCCTCGGCTGTACGCGAGGGGCGCGGTTCTTTTGTCAAGACCG	540						
QY	541	ACCTGTCCGCTGCTGAATGAATGAACTGAGGAGCGCGGCTATCTGTGCTGCCA	600						
Db	541	ACCTGTCCGCTGCTGAATGAATGAACTGAGGAGCGCGGCTATCTGTGCTGCCA	600						
QY	601	CGAGCGGCTTCTTGGCGAGCTGTCTGACGTTGCTGAAAGCGGAAGGACTGGC	660						
Db	601	CGAGCGGCTTCTTGGCGAGCTGTCTGACGTTGCTGAAAGCGGAAGGACTGGC	660						
QY	661	TGCTATTGGGGAAGTGCAGGCGAGGATCTCTGTCTCATCTCACCTTGTCTTCCGAGA	720						
Db	661	TGCTATTGGGGAAGTGCAGGCGAGGATCTCTGTCTCATCTCACCTTGTCTTCCGAGA	720						
QY	721	AAGTATCCATCATCGGCTGATGCAATGCGCGGCTGCTATGCTGTGCTGCTGCTGCC	780						
Db	721	AAGTATCCATCATCGGCTGATGCAATGCGCGGCTGCTATGCTGTGCTGCTGCTGCC	780						
QY	781	CATTGCAACCAAGCGAAACATCGATCGAGCGAGCACTGCTGATGGAAGCGGTC	840						
Db	781	CATTGCAACCAAGCGAAACATCGATCGAGCGAGCACTGCTGATGGAAGCGGTC	840						
QY	841	TTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCCAGCCGAACTGTTCG	900						
Db	841	TTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCCAGCCGAACTGTTCG	900						
QY	901	CCAGGCTCAAGCGCGGATGCCCCGAGGAGTCTGCTGACCATGCGCATGCTGCT	960						
Db	901	CCAGGCTCAAGCGCGGATGCCCCGAGGAGTCTGCTGACCATGCGCATGCTGCT	960						
QY	961	GCTTCCCGAATATCATGTGGAAATGGCCGCTTTTCTTGGATTATCGACTGTGSCCGGC	1020						

Db	2041	CAGGACCTCGTCGGCTGCGAAGCGCCCCCGGGGCGGTTCTTGTACACCATGACACCTGC	2100
Qy	2101	GGCAGCTCGGACCTTTACTTTGGTCACGAGGCATGCCGATGTCTATTCGGTGGCCCGCGCG	2160
Db	2101	GGCAGCTCGGACCTTTACTTTGGTCACGAGGCATGCCGATGTCTATTCGGTGGCCCGCGCG	2160
Qy	2161	GGCGACAGCAGGGGAGCGTACTCTCTCCGCCAGGCGCGTCTCCTACTTTGAAGGCTCTTCG	2220
Db	2161	GGCGACAGCAGGGGAGCGTACTCTCTCCGCCAGGCGCGTCTCCTACTTTGAAGGCTCTTCG	2220
Qy	2221	GGGSGTCCACTGCTCTGCCCTCGGGGACGGTGTGGGCATCTTTGGGCTCCGGTGTGC	2280
Db	2221	GGCGGTCCACTGCTCTGCCCTCGGGGACGGTGTGGGCATCTTTGGGCTCCGGTGTGC	2280
Qy	2281	ACCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCCTCGAGTCTATGGAAACCACTATG	2340
Db	2281	ACCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCCTCGAGTCTATGGAAACCACTATG	2340
Qy	2341	CGGTCCCCTGTTTCA CGGACAACTCGTCTCCCTCGGCGGTACCGACGACATTTCCAGTG	2400
Db	2341	CGGTCCCCTGTTTCA CGGACAACTCGTCTCCCTCGGCGGTACCGACGACATTTCCAGTG	2400
Qy	2401	GCCCATCTACACGCCCTACTCTGTAGCGGCAAGAGCACTAAGTGTCCGGCTGCGTATGCA	2460
Db	2401	GCCCATCTACACGCCCTACTCTGTAGCGGCAAGAGCACTAAGTGTCCGGCTGCGTATGCA	2460
Qy	2461	GCCCAAGGTTAAGGTGCTTGCTCTGAAACCGCTCCGTCCGCCGACCCCTAGGTTTCGGG	2520
Db	2461	GCCCAAGGTTAAGGTGCTTGCTCTGAAACCGCTCCGTCCGCCGACCCCTAGGTTTCGGG	2520
Qy	2521	GGGTATGTCTAAGGCAATGGTATCGACCTTAACATCAGAACCGGGGTAAAGCAACATC	2580
Db	2521	GGGTATGTCTAAGGCAATGGTATCGACCTTAACATCAGAACCGGGGTAAAGCAACATC	2580
Qy	2581	ACCACGGGTGCCCCCATCAGTACTCCACCTATGGCAAGTTTCTTGGCGACGGTGGTGC	2640
Db	2581	ACCACGGGTGCCCCCATCAGTACTCCACCTATGGCAAGTTTCTTGGCGACGGTGGTGC	2640
Qy	2641	TCGGGGGCGCCTATGACATCATATATGTGATGTGCGCACCTCAACTGACTCGACCACT	2700
Db	2641	TCGGGGGCGCCTATGACATCATATATGTGATGTGCGCACCTCAACTGACTCGACCACT	2700
Qy	2701	ATCCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTCGTG	2760
Db	2701	ATCCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGGCTGGAGCGGACTCGTCGTG	2760
Qy	2761	CTCGCACCGCTACGCCTCCGGGATCGGTACCGTGTCCACATCCAAACATCGAGGAGGTG	2820
Db	2761	CTCGCACCGCTACGCCTCCGGGATCGGTACCGTGTCCACATCCAAACATCGAGGAGGTG	2820
Qy	2821	GCTGTGTCCAGACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCCATCGAGACCATC	2880
Db	2821	GCTGTGTCCAGACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCCATCGAGACCATC	2880
Qy	2881	AAGGGGGAGGCACCTCATTTTCTGGCAATCCAAAGAAGAAATGTGATGAGCTCGCGCG	2940
Db	2881	AAGGGGGAGGCACCTCATTTTCTGGCAATCCAAAGAAGAAATGTGATGAGCTCGCGCG	2940
Qy	2941	AAGCTGTCCGCGCTCGGACTCAATGCTGTAGCATATTACGGGGCCTTGATGTATCCGTC	3000
Db	2941	AAGCTGTCCGCGCTCGGACTCAATGCTGTAGCATATTACGGGGCCTTGATGTATCCGTC	3000
Qy	3001	ATACCAACTAGCGGAGAGCTCATTTGCTGTAGCAACGGACGCTCTAATGACGGGCTTTACC	3060
Db	3001	ATACCAACTAGCGGAGAGCTCATTTGCTGTAGCAACGGACGCTCTAATGACGGGCTTTACC	3060
Qy	3061	GGCGATTTCGACTCAGTGATCGACTGCAATACATGTGTCAACCCAGACAGTCCACTTCAG	3120
Db	3061	GGCGATTTCGACTCAGTGATCGACTGCAATACATGTGTCAACCCAGACAGTCCACTTCAG	3120
Qy	3121	CTGACCCCGACCTTCACCATTTAGACGACGACCGTGGCCACAGACGGGTGTCACGCTCG	3180
Db	3121	CTGACCCCGACCTTCACCATTTAGACGACGACCGTGGCCACAGACGGGTGTCACGCTCG	3180

QY	3181	CAGCGGAGGACGAGACTGTTAGGCGCAGGATGGGCATTTACAGGTTTGTGATCTCCAGGA	3240
Db	3181	CAGCGGAGGACGAGACTGTTAGGCGCAGGATGGGCATTTACAGGTTTGTGATCTCCAGGA	3240
QY	3241	GAACGGCCCTCGGGCATGTTTCGATTTCTTCGGTTCGTGCGAGTGTATGACGCGGCTGT	3300
Db	3241	GAACGGCCCTCGGGCATGTTTCGATTTCTTCGGTTCGTGCGAGTGTATGACGCGGCTGT	3300
QY	3301	GCTTGTACGAGCTCACGCGCCGCGAGACCTCAGTTAGTTTCGGGCTTACTTAAACACA	3360
Db	3301	GCTTGTACGAGCTCACGCGCCGCGAGACCTCAGTTAGTTTCGGGCTTACTTAAACACA	3360
QY	3361	CCAGGTTGCCCTCTGCGAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTTC	3420
Db	3361	CCAGGTTGCCCTCTGCGAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTTC	3420
QY	3421	ACCCATAGACGCCCATTTCTTGTGCCAGACTAAGCAGGACGAGAGCAACTTCCCTTAC	3480
Db	3421	ACCCATAGACGCCCATTTCTTGTGCCAGACTAAGCAGGACGAGAGCAACTTCCCTTAC	3480
QY	3481	CTGGTAGCATACGAGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCAATCGTGGAC	3540
Db	3481	CTGGTAGCATACGAGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCAATCGTGGAC	3540
QY	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCCTACGCTCAACGGGCAACGCCCTCTGTG	3600
Db	3541	CAAAATGTGAAGTGTCTCATACGGCTAAAGCCTACGCTCAACGGGCAACGCCCTCTGTG	3600
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QY	3661	ATGGCATGCATCTCGCTCACCTCGGAGGTCGTCAACGAGCACCTGGGTGCTGTAGGCGGA	3720
Db	3661	ATGGCATGCATCTCGCTCACCTCGGAGGTCGTCAACGAGCACCTGGGTGCTGTAGGCGGA	3720
QY	3721	GTCTTAGCAGCTCTGGCCGCGTATTGCCCTGCAACACGAGCAGCGTGTCTTGTGGGAGG	3780
Db	3721	GTCTTAGCAGCTCTGGCCGCGTATTGCCCTGCAACACGAGCAGCGTGTCTTGTGGGAGG	3780
QY	3781	ATCATCTTGTCCGAAAGCGCGGCATCATTCGCGACAGGAAAGTCTCTTACCGGGAGTTC	3840
Db	3781	ATCATCTTGTCCGAAAGCGCGGCATCATTCGCGACAGGAAAGTCTCTTACCGGGAGTTC	3840
QY	3841	GATGAGATGGAAGTGTGCGCTCACACTCCCTTACATCGAACAGGGAATGCACTCGCC	3900
Db	3841	GATGAGATGGAAGTGTGCGCTCACACTCCCTTACATCGAACAGGGAATGCACTCGCC	3900
QY	3901	GAACAATTCAACAGAGAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGGCT	3960
Db	3901	GAACAATTCAACAGAGAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGGCT	3960
QY	3961	GCTGCTCCCGTGTGGAAATCCAAAGTGGCGGACCTTCGAAGCCCTCTGGGCGAAGCATATG	4020
Db	3961	GCTGCTCCCGTGTGGAAATCCAAAGTGGCGGACCTTCGAAGCCCTCTGGGCGAAGCATATG	4020
QY	4021	TGGAAATTCATACGCGGGATACATAATTTAGCAGGCTTGTCCACTGCTGCTGGAAACCC	4080
Db	4021	TGGAAATTCATACGCGGGATACATAATTTAGCAGGCTTGTCCACTGCTGCTGGAAACCC	4080
QY	4081	GGATAGCATCACTGATGGGATTCACAGCCCTCTATCACACGCGGCTCACCAACCAACAT	4140
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QY	4141	ACCTCTGTTTAACATCTCTGGGGGATGGGTGCGCGCCCAACTTGTCTCTCCAGCGCT	4200
Db	4141	ACCTCTGTTTAACATCTCTGGGGGATGGGTGCGCGCCCAACTTGTCTCTCCAGCGCT	4200
QY	4201	GCTTCTGCTTTCGTAGCGCGGCATCGCTGGAGCGGCTGTGGAGCATAGGCTTCGGG	4260
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 6361 CTGGAAGACACTGAGACACCAATTCACACCACTCATGGCAAAATGAGGTTTCTG 6420
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 6421 GTCCACACAGAGAGGGGGCGGAGCGAGCTCGCTTATCGTATTCACAGTTGGG 6480

Db	64721	GTCCAAACAGAGAAAGGGGGCCGCAAGCAGCTCGCCTTATCGTATTCACAGATTTGGGG	6480
QY	6481	GTTCTGTGTGCGAGAAAATGGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTG	6540
Db	6481	GTTCTGTGTGCGAGAAAATGGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTG	6540
QY	6541	ATGGGCTCTTCATACGGATTCGAATFACCTCTCTCTGGACACGGCGTCCAGTTCCTGGTGAAT	6600
Db	6541	ATGGGCTCTTCATACGGATTCGAATFACCTCTCTCTGGACACGGCGTCCAGTTCCTGGTGAAT	6600
QY	6601	GCCTGGAAGCGGAGAAATGCCCTATGGCTTCGCAATGACACCCGCTGTTTGACTCA	6660
Db	6601	GCCTGGAAGCGGAGAAATGCCCTATGGCTTCGCAATGACACACCCGCTGTTTGACTCA	6660
QY	6661	ACGCTCACTGAGAATGACATCCGCTGTTGAGAGTCAATCTACCAATGTGTCACTTGGCC	6720
Db	6661	ACGCTCACTGAGAATGACATCCGCTGTTGAGAGTCAATCTACCAATGTGTCACTTGGCC	6720
QY	6721	CCCGAAGCCAGACGGGCAATAGGTTCGCTCACAGACGGCTTTACATCGGGGCCCCCTG	6780
Db	6721	CCCGAAGCCAGACGGGCAATAGGTTCGCTCACAGACGGCTTTACATCGGGGCCCCCTG	6780
QY	6781	ACTAAATCTAAAGGCGAAGTCCGCTATCCCGTTCGCGGCGAGCGGTGTACTGACG	6840
Db	6781	ACTAAATCTAAAGGCGAAGTCCGCTATCCCGTTCGCGGCGAGCGGTGTACTGACG	6840
QY	6841	ACCAGCTGGGTAATACCTTCACATGTTACTTTGAAGCCGCTCGGCCCTGTCGAGTCCG	6900
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QY	6901	AGCTCCAGACTGCGAGTTCGTATGCGGACGACCTTGTCTGTTATCTGTGAAAGC	6960
Db	6901	AGCTCCAGACTGCGAGTTCGTATGCGGACGACCTTGTCTGTTATCTGTGAAAGC	6960
QY	6961	GCGGGACCCACAGACGACGAGCGCTACGGCCCTTCAGCGAGGTATGACTAGATAC	7020
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QY	7021	TCTGCCCCCTTGGGACCCGCCAAACAGAAATACGACTTGAGTTGATAACATCATGC	7080
Db	7021	TCTGCCCCCTTGGGACCCGCCAAACAGAAATACGACTTGAGTTGATAACATCATGC	7080
QY	7081	TCCTCCATGTGTCACTCGGACGATGCAATCTGGCAAAAGGCTGTACTCTCACCCGT	7140
Db	7081	TCCTCCATGTGTCACTCGGACGATGCAATCTGGCAAAAGGCTGTACTCTCACCCGT	7140
QY	7141	GACCCACACACCCCTTCGCGGGCTGGTGGGACAGCTAGACACACTCCAGTCAAT	7200
Db	7141	GACCCACACACCCCTTCGCGGGCTGGTGGGACAGCTAGACACACTCCAGTCAAT	7200
QY	7201	TCCTGGCTAGGCAACATCATATGATGCGCCACCTTGTGGCAAGGATGATCTGATG	7260
Db	7201	TCCTGGCTAGGCAACATCATATGATGCGCCACCTTGTGGCAAGGATGATCTGATG	7260
QY	7261	ACTCATTTCTCTCCATCTTCTAGCTCAGGAACAACTTTGAAAAGCCCTAGATTCTAG	7320
Db	7261	ACTCATTTCTCTCCATCTTCTAGCTCAGGAACAACTTTGAAAAGCCCTAGATTCTAG	7320
QY	7321	ATCTACGGGGCTGTACTCCATTCAGGCCACTTGACCTCAGATCATTCACAGACTC	7380
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QY	7381	CATGGCCTTAGGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
Db	7381	CATGGCCTTAGGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
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Db	7441	TCATGCCCTCAGGAACCTTGGGGTACCGCCCTTGCAGTCTGGAGACATCGGCCACAGT	7500
QY	7501	GTCGCGCTTAGGCTACTGTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTTC	7560
Db	7501	GTCGCGCTTAGGCTACTGTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTTC	7560

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DB	7561	AACTGGGCAGTAAGAGCAACAACTCACTCCAATCCCGGCTGGTCCCAAGTTGGAT	7620
QY	7621	TTATCCAGCTGGTTGGTTGCTGCTTACAGCGGGGAGACATATATACAGCCCTGTCTCGT	7680
DB	7621	TTATCCAGCTGGTTGGTTGCTGCTTACAGCGGGGAGACATATATACAGCCCTGTCTCGT	7680
QY	7681	GCCGAGACCCCGCTGGTTCAATGTGTCCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT	7740
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QY	7741	CTACTCCCAACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT	7800
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QY	7801	TTTCCCTCTTTTTTTTCTTT	7860
DB	7801	TTTCCCTCTTTTTTTTCTTT	7860
QY	7861	TTTTTCCTCTTTTTTTTCTTTTTTTCTTTTCTTTTCTTTTCTTTTCTCTTTTT	7920
DB	7861	TTTTTCCTCTTTTTTTTCTTTTTTTCTTTTCTTTTCTTTTCTTTTCTCTTTTT	7920
QY	7921	TAGCTGTGAAGTCCGTGAGCGCTGTGACTGCAGAGAGTGTCTGATCTGGCCTCTCTGC	7980
DB	7921	TAGCTGTGAAGTCCGTGAGCGCTGTGACTGCAGAGAGTGTCTGATCTGGCCTCTCTGC	7980
QY	7981	AGATCAAGT 7989	
DB	7981	AGATCAAGT 7989	
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; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 7			
; LENGTH: 8001			
; TYPE: DNA			
; ORGANISM: Hepatitis C virus			
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; LOCATION: (1)..(341)			
; OTHER INFORMATION: construct 1389/NS3-3'/wt			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (342)..(1193)			
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; FEATURE:			
; NAME/KEY: RBS			
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; OTHER INFORMATION: encephalomyocarditis virus			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1813)..(7770)			
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3-5B			
; FEATURE:			
; NAME/KEY: 3'UTR			
; LOCATION: (7771)..(8001)			

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AUTHORS: Krner, Frank
AUTHORS: Koch, Jan-Oliver
AUTHORS: Herian, Ulrike
AUTHORS: Theilmann, Lorenz
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QY	61	TTTTCAGCAGAAAGCTTAGCCATGGCGTGTAGTATGATGTCGACGCTCCAGGAC	120
Db	61	TTTTCAGCAGAAAGCTTAGCCATGGCGTGTAGTATGATGTCGACGCTCCAGGAC	120
QY	121	CCCCCTCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTCGAG	180
Db	121	CCCCCTCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTCGAG	180
QY	181	GAGCAGCGGTCTTTCTTGGATCAACCCGCTCAATGCCCTGGAGATTGGCGGTGCCCC	240
Db	181	GAGCAGCGGTCTTTCTTGGATCAACCCGCTCAATGCCCTGGAGATTGGCGGTGCCCC	240
QY	241	GCAGACTGTAGCCGAGTAGTGTGGTTCGGAAGCGCTTGTGGTACTGCTGTATGG	300
Db	241	GCAGACTGTAGCCGAGTAGTGTGGTTCGGAAGCGCTTGTGGTACTGCTGTATGG	300
QY	301	GTGCTTCGGAGTCCCGGGAGTCTGTAGACGCTGCACATGAGCAGAACTCTAAAC	360
Db	301	GTGCTTCGGAGTCCCGGGAGTCTGTAGACGCTGCACATGAGCAGAACTCTAAAC	360
QY	361	CTCAAGAGAAAACCAAA-----GGCGCGCATGATTGAACAGATGATTGC	408
Db	361	CTCAAGAGAAAACCAAA-----GGCGCGCATGATTGAACAGATGATTGC	420
QY	409	ACGAGGTCTCCGCGCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCACACAGA	468
Db	421	ACGAGGTCTCCGCGCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCACACAGA	480
QY	469	CAATCGGTGTCTGATCGCGCGTGTTCGGCTGTACGCGAGGGCGCGCGGTCTTT	528
Db	481	CAATCGGTGTCTGATCGCGCGTGTTCGGCTGTACGCGAGGGCGCGCGGTCTTT	540
QY	529	TTGTCAAGACCGACTGTCCGCTGCTGATGAATGAATGACAGCAGCAGCGCGCTAT	588
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QY	589	CGTGTGCGCAGCAGCGCGCTTCTTGGCAGCTGTGCTCGACGTTGTCACTGAAGCGG	648
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QY	649	GAAGGACTGTGGTCTATTGGGCGAAGTCCCGGGCAGGATCTCTGTATCTCACTTGG	708
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QY	709	CTCTCCGAGAAAGTATCCATCATGCTGATGCGGGCTGCAATGAGCTTGTATC	768
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841	TGGAAGCCGGTCTTTGTCGATCAGATGATCTGAGCAAGACATCAGGGGTCCGGCAG	900
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1069	TTGCTGAAGAGCTTGGCGGCAATGGCTGACCGCTTCTGCTGTATACGGTATCGCG	1128
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1261	ACGTTACTGCGCGAAGCGCTTGAATAGGCGGTGTCGCTTGTCTATATGTTATTT	1320
1309	TCACACATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTTCTG	1368
1321	TCACACATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTTCTG	1380
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1381	ACGAGCAATTCCTAGGGGTCTTCCCTCTCGCAAGAAATGCAAGTCTGTTCAATGTC	1440
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1441	GTGAAGAGCAGTTCCTCTGAGAGCTTCTTGAAGACAAACAACTGTAGCAGCCCTT	1500
1489	TGCAGGAGCGGAACCCCACTTGGCGACAGGTGCTTCCGCGCAAAAGCCAGTGA	1548
1501	TGCAGGAGCGGAACCCCACTTGGCGACAGGTGCTTCCGCGCAAAAGCCAGTGA	1560
1549	TAAGATACCTGCAAGGGCGCAACCCAGTGCACAGTGTGAGTTGATAGTTG	1608
1561	TAAGATACCTGCAAGGGCGCAACCCAGTGCACAGTGTGAGTTGATAGTTG	1620
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2341 GAAACCACTATCGGCTCCCGGCTTTACGAGCAACTCGTCCCGGCGGCACTTAAGTGTCCG 2400
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Db	6301	TATGGGGCAAAAGGAGCGTCCGGAACCTATCCAGCAAGGCGGTAAACCAATCCGCTCCGCTG	6360
Qy	6349	TGGAAGGACTTGTCTGTGAAGACACTGAGACACCAATTGACACCAACCATATGCGCAAAAAAT	6408
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Db	6421	GAGGTTTTCTCGTCCACACAGAAAGGGGGCGCAGCAGCGTCCGCTTATGCTATTC	6480
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Qy	6529	CCTCAGGCGTGATGGGCTCTTCATCGGATTCGAATCTCTCTCTGACAGCGGCTCGAG	6588
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Qy	6649	TGTTTTGACTCAACGGTCACTGAGAATGACATCCGTGTTGAGGAGTCAATCTACCAATGT	6708
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Qy	6709	TGTGACTTTGCCCGCCGACAGCGCCATTAAGTTCGTCTCAGAGCGGCTTTACATC	6768
Db	6721	TGTGACTTTGCCCGCCGACAGCGCCATTAAGTTCGTCTCAGAGCGGCTTTACATC	6780
Qy	6769	GGGGGGCCCCGTGACTAATTTCAAAGGCGAGAACTGCGGCTATCGCGGTCCGCGCGAGC	6828
Db	6781	GGGGGGCCCCGTGACTAATTTCAAAGGCGAGAACTGCGGCTATCGCGGTCCGCGCGAGC	6840
Qy	6829	GGTGTACTGACGACCGAGCTGCGGTAATACCTCACAATGTTACTTTGAAGCGCTCGCGCC	6888
Db	6841	GGTGTACTGACGACCGAGCTGCGGTAATACCTCACAATGTTACTTTGAAGCGCTCGCGCC	6900
Qy	6889	TGTCGAGCTTCGGAAGCTCCAGGACTCGACGATGCTCGATGCGGAGACGACCTTGCTGTT	6948
Db	6901	TGTCGAGCTTCGGAAGCTCCAGGACTCGACGATGCTCGATGCGGAGACGACCTTGCTGTT	6960
Qy	6949	ATCTGTGAAGCGCGGGACCCAAAGAGGACGAGCGAGCCTACGGGCTTACAGGAGCT	7008
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Db	7021	ATGACTAGATACTCTGCCCGCCCTGGGGACCGCGCCCAACACAGATACGACTTGCAGTTG	7080
Qy	7069	ATAACATCATGCTCTCCAAATGTGTGTCGCGGCGACGATGCAATCTGGCAAGGGTGTAC	7128
Db	7081	ATAACATCATGCTCTCCAAATGTGTGTCGCGGCGACGATGCAATCTGGCAAGGGTGTAC	7140
Qy	7129	TATCTCACCCGCTGACCCACACCCCTTTCGCGGGTTCGCTGGGAGACGACTTAGACAC	7188
Db	7141	TATCTCACCCGCTGACCCACACCCCTTTCGCGGGTTCGCTGGGAGACGACTTAGACAC	7200
Qy	7189	ACTCCAGTCAATTCTCGGTAGGCAACATCATGTATGCGCCCACTTGTGGCAAGG	7248
Db	7201	ACTCCAGTCAATTCTCGGTAGGCAACATCATGTATGCGCCCACTTGTGGCAAGG	7260
Qy	7249	ATGATCCTGATCACTTCTTCTCCATCTTCTAGCTCAGGAACAATCTGAAAAAGCC	7308
Db	7261	ATGATCCTGATCACTTCTTCTCCATCTTCTAGCTCAGGAACAATCTGAAAAAGCC	7320
Qy	7309	CTAGATTGTTCAGATCTACGGGCGCTTACTCCATTGAGGCACTTGACCTACCTAGATC	7368
Db	7321	CTAGATTGTTCAGATCTACGGGCGCTTACTCCATTGAGGCACTTGACCTACCTAGATC	7380

QY	7369	ATTCAACGACTCCATGCGCTTAGCGCATTTTTCATCTCCATAGTTACTCTCCAGGTGAGATC	7429
Db	7381	ATTCAACGACTCCATGCGCTTAGCGCATTTTTCATCTCCATAGTTACTCTCCAGGTGAGATC	7440
QY	7429	AATAGGTGGCTTCATCGCTCAGAAACTTTGGGGTACCGCCCTTGGAGTCTGGAGACAT	7488
Db	7441	AATAGGTGGCTTCATCGCTCAGAAACTTTGGGGTACCGCCCTTGGAGTCTGGAGACAT	7500
QY	7489	CGGGCCAGAAAGTGTCCGCGCTAGGCTACTGTCCACGGGGGAGGGCTGCCACTTTGTGGC	7548
Db	7501	CGGGCCAGAAAGTGTCCGCGCTAGGCTACTGTCCACGGGGGAGGGCTGCCACTTTGTGGC	7560
QY	7549	AAGTACTCTTCAACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGG	7608
Db	7561	AAGTACTCTTCAACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGG	7620
QY	7609	TCCAGATTGATTTATCCAGCTGGTTGCTGTGTTTACAGCGGGGAGACATATATCAC	7668
Db	7621	TCCAGATTGATTTATCCAGCTGGTTGCTGTGTTTACAGCGGGGAGACATATATCAC	7680
QY	7669	AGCCTGTCTCGTCCCGACCCCGCTGCTCATGTGTGCTACTCCTACTCTTCTGTAGGG	7728
Db	7681	AGCCTGTCTCGTCCCGACCCCGCTGCTCATGTGTGCTACTCCTACTCTTCTGTAGGG	7740
QY	7729	GTAGGCATCTATCTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGG	7788
Db	7741	GTAGGCATCTATCTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGG	7800
QY	7789	CCATCTCGTTTTTTTCCCTTT	7848
Db	7801	CCATCTCGTTTTTTTCCCTTT	7860
QY	7849	TTTTCTCCTTTTTTTTTCTCTTTTTTTTCCCTTTCTTTCTTTCTTTCTTTCTTTCTTT	7908
Db	7861	TTTTCTCCTTTTTTTTTCTCTTTTTTTTCCCTTTCTTTCTTTCTTTCTTTCTTTCTTT	7920
QY	7909	CCTAGTCAAGCTAGCTGTGAAGGTCCGTGAGCCGCTTTGACTGCAGAGAGTGTCTGATAC	7968
Db	7921	CCTAGTCAAGCTAGCTGTGAAGGTCCGTGAGCCGCTTTGACTGCAGAGAGTGTCTGATAC	7980
QY	7969	TGSCCTCTCTGCAGATCAAGT	7989
Db	7981	TGSCCTCTCTGCAGATCAAGT	8001

RESULT 3

US-09-539-601-22

; Sequence 22, Application US/09539601C

; Patent No. 6630343

; GENERAL INFORMATION:

; APPLICANT: Bartenschlager, Ralf FW

; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System

; FILE REFERENCE: all sequences

; CURRENT APPLICATION NUMBER: US/09/539,601C

; EARLIER FILING DATE: 2001-08-30

; EARLIER FILING DATE: 1999-04-03

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 22

; LENGTH: 8001

; TYPE: DNA

; ORGANISM: Hepatitis C virus

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: (1)..(341)

; OTHER INFORMATION: construct I389/NS3-3'/5.1

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (342)..(1193)

; OTHER INFORMATION: hepatitis C virus core - neomycin

; OTHER INFORMATION: phosphotransferase fusion protein

; FEATURE:

NAME/KEY: RBS
LOCATION: (1202)..(1812)
OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1813)..(7770)
OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
OTHER INFORMATION: of cell culture-adapted clone no. 5.1
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (7771)..(8001)
US-09-539-601-22

Query Match 99.5%; Score 7949.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7978; Conservative 0; Mismatches 11; Indels 12; Gaps 1;

QY 1 GCCAGCCCCGATTGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAACTACTG 60
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QY 61 TCTTCAAGCAGAAAGCGTTAGCCATGGCGTTAGTATGATGTCTGTCAGCCTCCAGGAC 120
DB 61 TCTTCAAGCAGAAAGCGTTAGCCATGGCGTTAGTATGATGTCTGTCAGCCTCCAGGAC 120
QY 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGAACCCTGTGAGTACACCGGAATTGCCAG 180
DB 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGAACCCTGTGAGTACACCGGAATTGCCAG 180
QY 181 GAGCAGCGGTCTTCTTGGATCAACCGCTCAATCGCTGGAGATTGGCGGTGCCCCC 240
DB 181 GAGCAGCGGTCTTCTTGGATCAACCGCTCAATCGCTGGAGATTGGCGGTGCCCCC 240
QY 241 GCGAGACTGTACCGAGTAGTGTGGGTGCGAAGAGCGCTTGTGTACTGCTGTATAG 300
DB 241 GCGAGACTGTACCGAGTAGTGTGGGTGCGAAGAGCGCTTGTGTACTGCTGTATAG 300
QY 301 GTGCTTTCGAGTCCCGGAGGTCTGCTAGACCGGTGACCATGAGCAGAACTCTTAAC 360
DB 301 GTGCTTTCGAGTCCCGGAGGTCTGCTAGACCGGTGACCATGAGCAGAACTCTTAAC 360
QY 361 CTCAGAGAAACCAAA-----GGGCGCGCATGATTGAACAGATGGATTGC 408
DB 361 CTCAGAGAAACCAAAACCAACCGGCGCGCATGATTGAACAGATGGATTGC 420
QY 409 ACGCAGGTCTCCGGCGCGCTTGGGTGAGAGGCTATTTCGGCTATGATCGGCAACAG 468
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QY 469 CAATCGGCTGTGATGCGCGCGTGTTCGGCTGTGAGCGAGGGCGCGGTTCTTT 528
DB 481 CAATCGGCTGTGATGCGCGCGTGTTCGGCTGTGAGCGAGGGCGCGGTTCTTT 540
QY 529 TTGTCAGACCGACTGTCGGTCCCTGAATGAATGACGAGCAGCGCGGCTAT 588
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QY 589 CGTGGCTGGCCACGACGGCGCTTCCTTTCGAGCTGTGCTGAGCTGTGATGAGAGGG 648
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DB 7621 TCCAGTTGGATTTATCCAGCTGTTCTGCTTACAGCGGGGAGACATATATCAC 7680
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DB 7801 CCATCTGTTTTTTCCTTT 7860
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DB 7921 CCTAGTCACCGCTAGCTGTGAAGGCTCCGTGAGCGGCTTGAAGTCCGTGAGCGGCTGCTGATAC 7980
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DB 7981 TGGCCTCTCTGCAGATCAAGT 8001

RESULT 4

US-09-539-601-16
; Sequence 16, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/9-13F
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase
; OTHER INFORMATION: fusion protein
; FEATURE:
; NAME/KEY: RBS

LOCATION: (1202)..(1812)
OTHER INFORMATION: internal ribosome entry site from
OTHER INFORMATION: encephalomyocarditis virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1813)..(7770)
OTHER INFORMATION: hepatitis C virus nonstructural protein NS3-5B;
OTHER INFORMATION: carries cell culture-adaptive mutations from clone
OTHER INFORMATION: 9-13F
FEATURE:
NAME/KEY: 3'UTR
LOCATION: (7771)..(8001)
US-09-539-601-16

Query Match 99.4%; Score 7947.8; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7977; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

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QY 61 TCTTCAAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTGCTGTCAGCCCTCCAGGAC 120
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QY 121 CCCCCCTCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180
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QY 181 GAGCAGCGGTCTTTCTTGGATCAACCCGCTCAATGCCCTGGAGATTGGCGGTGCCCCC 240
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2221 AAGGGCTCTTTCGGGGGCTCCACTGTCTGCCCTCGGGGCACTGTGGGCATCTTTCCG 2280
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3961 CAAAGCGAGGCTGCTGCTCCCTGTGTGGAATCAAGTGGCGGACCTTCAAGGCTTCTGG 4020
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4021 GCGAGCATATGTGGAATTTTCATCAGCGGATACAAATATTTAGCGGCTTGTCCACTCTG 4080
4069 CTTGGCAACCCCGCATAGCATCATGTGGAATTCAGGCTCTATACAGCGCGCTC 4128

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4129	Qy	ACAACCA	ATACCTCTCT	TTTAACTACCT	CTGGGGGATGGT	CGCCCAACTT	4188	Db	TGCGGGCCGAA	CCGGACGTAG	CAGTGCCT	CACCTTCCAT	GTCTCACCGACCCCTCC	CAACATT	5280
4141	Db	ACAACCA	ATACCTCTCT	TTTAACTACCT	CTGGGGGATGGT	CGCCCAACTT	4200	Qy	ACGCGGAGAC	CGGCTAAG	CGCTAGGCT	TGGCCAGGGAT	CTCCCCCTCT	CTTTGGCCAGCTCA	5328
4189	Qy	CCCTCC	AGCGCTCT	CTGCTTCT	GTAGGCGCCG	GCATCGCT	4248	Db	ACGCGGAGAC	CGGCTAAG	CGCTAGGCT	TGGCCAGGGAT	CTCCCCCTCT	CTTTGGCCAGCTCA	5340
4201	Db	CCCTCC	AGCGCTCT	CTGCTTCT	GTAGGCGCCG	GCATCGCT	4260	Qy	TCAGCTAG	CAGCTGT	CTGGCCCT	TCTTTGA	AGGCACTG	CACTACCGCTCAT	5388
4249	Qy	ATAGCCCT	TGGGAAAG	GTCTGTGGAT	TAATTTTGGC	AGGTAT	4308	Db	TCAGCTAG	CCAGCTGT	CTGGCCCT	TCTTTGA	AGGCACTG	CACTACCGCTCAT	5400
4261	Db	ATAGCCCT	TGGGAAAG	GTCTGTGGAT	TAATTTTGGC	AGGTAT	4320	Qy	CCGACGCT	GACCTCAT	CTGAGG	CCAACT	CTGTGG	CGGAGAGAT	5448
4309	Qy	CGCTCT	GTGGCTTT	TAAGTTC	ATGAGCGG	CGAGAT	4368	Db	CCGACGCT	GACCTCAT	CTGAGG	CCAACT	CTGTGG	CGGAGAGAT	5460
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4369	Qy	CTACTC	CTCTAT	CTCTC	CTCCCT	TGGGCG	4428	Db	ACCCGCGT	GGAGT	CAGAAA	TAAGT	AGTAA	TTTGGAC	5520
4381	Db	CTACTC	CTCTAT	CTCTC	CTCCCT	TGGGCG	4440	Qy	GAGGAG	GATGAG	GGGAG	TATCCG	TTC	CGGCGAGAT	5568
4429	Qy	CTGCGT	CGGCA	CGTGGG	CCGAGG	GGGCGT	4488	Db	GAGGAG	GATGAG	GGGAG	TATCCG	TTC	CGGCGAGAT	5580
4441	Db	CTGCGT	CGGCA	CGTGGG	CCGAGG	GGGCGT	4500	Qy	CCTCAG	CGATG	CCCATAT	TGGCAC	CGCCG	GATTACAA	5628
4489	Qy	TTTCGCT	CGCGGG	TAAAC	CACTCT	CCCC	4548	Db	CCTCAG	CGATG	CCCATAT	TGGCAC	CGCCG	GATTACAA	5640
4501	Db	TTTCGCT	CGCGGG	TAAAC	CACTCT	CCCC	4560	Qy	AAGGAC	CCCGA	CTACG	TCCCT	CAGTGT	CA	5688
4549	Qy	GCAGTG	TCAC	TACAT	CTCT	CTAGT	4608	Db	AAGGAC	CCCGA	CTACG	TCCCT	CAGTGT	CA	5700
4561	Db	GCAGTG	TCAC	TACAT	CTCT	CTAGT	4620	Qy	CCTC	CGAT	TCAC	ACTCT	CACG	AGGAGT	5748
4609	Qy	CAGTGA	TCAAC	GAGAC	TGCT	CCAC	4668	Db	CCTC	CGAT	TCAC	ACTCT	CACG	AGGAGT	5760
4621	Db	CAGTGA	TCAAC	GAGAC	TGCT	CCAC	4680	Qy	TCGTC	CTC	CGCG	AGT	CGCC	CAAA	5808
4669	Qy	GATTGA	TATG	CA	CGGT	GTG	4728	Db	TCGTC	CTC	CGCG	AGT	CGCC	CAAA	5820
4681	Db	GATTGA	TATG	CA	CGGT	GTG	4740	Qy	AGCG	CA	CGG	CAAC	CGG	CTCT	5868
4729	Qy	CGATTG	CGCG	AGT	CCCTCT	TTCT	4788	Db	AGCG	CA	CGG	CAAC	CGG	CTCT	5880
4741	Db	CGATTG	CGCG	AGT	CCCTCT	TTCT	4800	Qy	GTG	AGT	TCG	TACT	CTC	CAAT	5928
4789	Qy	GACGG	ATCAT	GAA	ACCA	CTGCC	4848	Db	GTG	AGT	TCG	TACT	CTC	CAAT	5940
4801	Db	GACGG	ATCAT	GAA	ACCA	CTGCC	4860	Qy	GAC	GGT	CTT	GGT	CTT	ACCG	5988
4849	Qy	GGTTC	ATAG	GAT	CGTGG	GGCT	4908	Db	GAC	GGT	CTT	GGT	CTT	ACCG	6000
4861	Db	GGTTC	ATAG	GAT	CGTGG	GGCT	4920	Qy	TCCT	TAC	AT	TG	GAT	CA	6048
4909	Qy	ATTAA	CGG	TAC	CA	CGG	4968	Db	TCCT	TAC	AT	TG	GAT	CA	6060
4921	Db	ATTAA	CGG	TAC	CA	CGG	4980	Qy	AT	CA	AT	CG	CA	CA	6108
4969	Qy	CTGTG	GGGGT	TGCT	GTG	AGG	5028	Db	AT	CA	AT	CG	CA	CA	6120
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5029	Qy	GTGAC	GGG	ATG	CA	CTG	5088	Db	CG	CA	CG	CC	CT	TG	6180
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5101	Db	TTTCA	CAG	AA	TG	AGT	5160	Qy	CT	AT	CG	CA	CG	CC	6288
5149	Qy	CGGAG	GAG	GT	CA	CA	5208	Db	CT	AT	CG	CA	CG	CC	6300
5161	Db	CGGAG	GAG	GT	CA	CA	5220								

6289 QY TATGGGCAAGGACCTCGGAACTTATCAGCAAGCCGTTAAACCAATCCGCTCGGTG 6348
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7189 QY ACTCCAGTCAATTCCTGGCTAGGCAACATCATATGTCGCCGCCACCTTGTGGCAAGG 7248
7201 Db ACTCCAGTCAATTCCTGGCTAGGCAACATCATATGTCGCCGCCACCTTGTGGCAAGG 7260
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7549 QY AAGTACTCTTCAACTGGSCAGTAAGGCAAGCTCAAACTCACTCAATCCCGGCTGG 7608
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7621 Db TCCCAGTTGGATTTATCCAGCTGGTTGCTGTTACAGCGGGGAGACATATATCAC 7680
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7681 Db AGCTGTCTGTCGCCGACCCCGCTGGTTCATGTGCTGCTACTCTCTTCTGTAGG 7740
7729 QY GTAGGCATCTATCTACTCCCAACCGATGAACGGGAGCTAAACCTCCAGGCCAATAGG 7788
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7789 QY CCATCTGTTTTTTTCCCTTT 7848
7801 Db CCATCTGTTTTTTTCCCTTT 7860
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7861 Db TTTTCTCCTTTTTTTTTCCTCTTTTTTTTTCCTTTTTTTCCTTTTGGTGCTCCATCTTAGC 7920
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7981 Db TGGCCTCTCTGCAGATCAAGT 8001

RESULT 5

US-09-539-601-28
; Sequence 28, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct 1389/NS3-3'/19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS

Tue Nov 2 14:02:16 2004

LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
; OTHER INFORMATION: of cell culture adapted clone no. 19
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7771)..(8001)
; US-09-539-601-28

Query Match 99.4%; Score 7941.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;
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1 GCCAGCCCCGATGGGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAACACTG 60
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409 ACGCAGGTTCTCCGCGCGCTTGGGTGGAGAGGCTATTCCGCTATGATCTGGGCAACAGA 468
421 ACGCAGGTTCTCCGCGCGCTTGGGTGGAGAGGCTATTCCGCTATGATCTGGGCAACAGA 480
469 CAATCGGCTGTGATGCGCGGCTTCCGCTGTGACGCGAGGCGCGCGGTCTTT 528
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901 CCGAATCTTTCGCGAGGCTCAAGGCGCATGCCGAGCGGAGGATCTCGTCGTCACCC 960
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1609 GAAAGATCAATGCTCTCTCAAGCGTATTAACAAAGGCGCTGAAGATGCGCAGAG 1668
1621 GAAAGATCAATGCTCTCTCAAGCGTATTAACAAAGGCGCTGAAGATGCGCAGAG 1680
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1909 GTCTCCACCGCAACAATCTTTCTTCTGGCGACCTGCTCAATGGCGTGTGTTGGAATGTC 1968

Db 1921 GTCTCCACCGCAACAATCTTTCTGGGACCTGGTCAATGGCGTGTGGACTGTC 1980
QY 1969 TATCATGTGTCGGCTCAAGACCTTGGCGGCCAAAGGCCCAATCAACCAATGTAC 2028
Db 1981 TATCATGTGTCGGCTCAAGACCTTGGCGGCCAAAGGCCCAATCAACCAATGTAC 2040
QY 2029 ACCAATGTGGACAGACCTGTGGCTGGCAAGGCCCGCGGCGGCTTCCTTGACA 2088
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RESULT 6
US-09-539-601-4
; Sequence 4, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8637
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I377/NS2-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1181)
; OTHER INFORMATION: HCV core-neomycin phosphotransferase fusion
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1190)..(1800)

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; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1801)..(8406)
; OTHER INFORMATION: hepatitis C virus NS2 - 5B
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; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (8407)..(8637)
; PUBLICATION INFORMATION:
; AUTHORS: Lohmann, Volker
; AUTHORS: Kriener, Frank
; AUTHORS: Koch, Jan-Oliver
; AUTHORS: Herian, Ulrike
; AUTHORS: Theilmann, Lorenz
; AUTHORS: Bartenschlager, Ralf
; TITLE: Replication of subgenomic hepatitis c virus RNAs in a
; TITLE: hepatoma cell line
; JOURNAL: Science
; VOLUME: 285
; PAGES: 110-113
; DATE: 1999-07-02
; US-09-539-601-4

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Db 3421 ACGCTCTGGGATCGGTCAACCTGCAATCCAAACATCGAGGAGTGGCTCTGTCCAGC 3480
Qy 2833 ACTGGAGAAATCCCTTTTATGGCAAAAGCCATCCCATCGAGACCATCAAGGGGGGAGG 2892
Db 3481 ACTGGAGAAATCCCTTTTATGGCAAAAGCCATCCCATCGAGACCATCAAGGGGGGAGG 3540
Qy 2893 CACCTCATTTTCTGCCATTCCAAGAAATGTGATGAGTCCGCCGCGGAGACTGTCCGGC 2952
Db 3541 CACCTCATTTTCTGCCATTCCAAGAAATGTGATGAGTCCGCCGCGGAGACTGTCCGGC 3600
Qy 2953 CTGGACTCAATGCTGATGATATTACCGGGGCTTGTATGATCCGTCATACCAACTAGC 3012
Db 3601 CTGGACTCAATGCTGATGATATTACCGGGGCTTGTATGATCCGTCATACCAACTAGC 3660
Qy 3013 GGAGAGTCAATCTCGTAGCAACGAGCTCTAATGACGGGCTTTTACCGGCGATTTGAC 3072
Db 3661 GGAGAGTCAATCTCGTAGCAACGAGCTCTAATGACGGGCTTTTACCGGCGATTTGAC 3720
Qy 3073 TCAGTATCGACTGCAATCATGTGTCCACGACAGTGTGACTTCCAGGCGGCTTACCGGCGATTTGAC 3780
Db 3721 TCAGTATCGACTGCAATCATGTGTCCACGACAGTGTGACTTCCAGGCGGCTTACCGGCGATTTGAC 3840
Qy 3133 TTCACCATTTGAGACGACCGCTGCGCAAGAGCGGCTGTACGCTCGGAGCGGCGGAGG 3192
Db 3781 TTCACCATTTGAGACGACCGCTGCGCAAGAGCGGCTGTACGCTCGGAGCGGCGGAGG 3840
Qy 3193 AGGACTGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGAGAACGGGCTCG 3252
Db 3841 AGGACTGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGAGAACGGGCTCG 3900
Qy 3253 GGCATGTTTCGATCTCTCGGTTCTGTGCGAGTGTATGACGCGGCTGTCTTGGTACGAG 3312
Db 3901 GGCATGTTTCGATCTCTCGGTTCTGTGCGAGTGTATGACGCGGCTGTCTTGGTACGAG 3960

QY	3313	CTACGCCGCCGAGACCTCAGTTAGTTTGGCGCTTACCTAAACACACACACAGGGTTGCC	3372	5041	GGCGCCCTAGTCTCGGGGTCTGTGCGCAGGATCTGCGTCGCGACGTGGCGCCAGGG	5100
Db	3361	CTACGCCGCCGAGACCTCAGTTAGTTTGGCGCTTACCTAAACACACACAGGGTTGCC	4020	4453	GAGGGGGTGTGCAGTGTGATGAACCGGCTGTAGGTTTGGTTTCCGGGGTGAACACAGTC	4512
QY	3373	GTCTGCCAGGACCACTCTGGAGTTCTGGGAGAGCGTCTTTTACAGGCGCTCACCCACATAGAC	3432	5101	GAGGGGGTGTGCAGTGTGATGAACCGGCTGTAGGTTTGGTTTCCGGGGTGAACACAGTC	5160
Db	4021	GTCTGCCAGGACCACTCTGGAGTTCTGGGAGAGCGTCTTTTACAGGCGCTCACCCACATAGAC	4080	4513	TCCCCCAGCAGCTATGTGCTGTAGAGCGAGCGTGTGAGCAGCGTGTCACTCAGATCTCTCT	4572
QY	3433	GCCCATTTCTTGTCCAGACTAAGCAGGAGGAGAGCACTTCCCTTACCTGTGTAGCATAC	3492	5161	TCCCCCAGCAGCTATGTGCTGTAGAGCGAGCGTGTGAGCAGCGTGTCACTCAGATCTCTCT	5220
Db	4081	GCCCATTTCTTGTCCAGACTAAGCAGGAGGAGAGCACTTCCCTTACCTGTGTAGCATAC	4140	4573	AGTCTTACCATCACTCAGCTGTGAAGGCTTTCACCACTGTGATCAACAGAGACTGTCTCC	4632
QY	3493	CAGGCTACGGTGTGCGCAGGCTCAGGCTCAGGCTCAGCTCCATCTGCGAGCAAAATGTGGAAG	3552	5221	AGTCTTACCATCACTCAGCTGTGAAGGCTTTCACCACTGTGATCAACAGAGACTGTCTCC	5280
Db	4141	CAGGCTACGGTGTGCGCAGGCTCAGGCTCAGGCTCAGCTCCATCTGCGAGCAAAATGTGGAAG	4200	4633	ACGCCATGTCCGGGTCTGTGGCTTAAGAGATGTTTGGGATTTGGGATTTGGATTTGACT	4692
QY	3553	TGTCTCATACGGTAAAGCTCAGCTGTGACGGGCGCAACGCCCTGTGTATAGGCTGGGA	3612	5281	ACGCCATGTCCGGGTCTGTGGCTTAAGAGATGTTTGGGATTTGGGATTTGGATTTGACT	5340
Db	4201	TGTCTCATACGGTAAAGCTCAGCTGTGACGGGCGCAACGCCCTGTGTATAGGCTGGGA	4260	4693	GATTTCAAGACCTGGCTCCAGTCCCAAGCTCTGCGCGGATTTGCGGGAGTCCCTCTCTTC	4752
QY	3613	GCGGTTCAAAACGAGGTTACTACCAACACCCCATTAACCAATACATCATGGCATCATG	3672	5341	GATTTCAAGACCTGGCTCCAGTCCCAAGCTCTGCGCGGATTTGCGGGAGTCCCTCTCTTC	5400
Db	4261	GCGGTTCAAAACGAGGTTACTACCAACACCCCATTAACCAATACATCATGGCATCATG	4320	4753	TCATGTCAAGCTGGGTACAAAGGAGTCTGCGGGGCGAGCGGCATCATGCAAAACCACTGC	4812
QY	3673	TCGGCTGACCTGAGGTCGTACAGACACCTGGGTGTGTAGCGGAGTCTTAGCAGCT	3732	5401	TCATGTCAAGCTGGGTACAAAGGAGTCTGCGGGGCGAGCGGCATCATGCAAAACCACTGC	5460
Db	4321	TCGGCTGACCTGAGGTCGTACAGACACCTGGGTGTGTAGCGGAGTCTTAGCAGCT	4380	4813	CCATGTGGAGCAGATACCCGACATGTGAAAAAAGGTTCCATGAGGATCTGTGGGCGCT	4872
QY	3733	CTGCGCGGATTTGCTGTGACAAACAGGAGCGGTGTCTATTGTGGCAGGATCATCTGTCC	3792	5461	CCATGTGGAGCAGATACCCGACATGTGAAAAAAGGTTCCATGAGGATCTGTGGGCGCT	5520
Db	4381	CTGCGCGGATTTGCTGTGACAAACAGGAGCGGTGTGTCTATTGTGGCAGGATCATCTGTCC	4440	4873	AGGACCTGTAGTAACAGCTGGCATGNAACATTCCTCCATTAACCGTACACACCGGCGCCC	4932
QY	3793	GGAAAGCGCGCATCATTTCCCGACAGGAAATGCTTTTACCGGAGTTCGATGAGATGGA	3852	5521	AGGACCTGTAGTAACAGCTGGCATGNAACATTCCTCCATTAACCGTACACACCGGCGCCC	5580
Db	4441	GGAAAGCGCGCATCATTTCCCGACAGGAAATGCTTTTACCGGAGTTCGATGAGATGGA	4500	4933	TGCACGCGCTCCCGCGCGCAAAATTTTCTAGGCGCTGTGGCGGGTGGTGTCTGAGAG	4992
QY	3853	GAGTGCCTCTCACACCTCCCTTACATCGAACAGGAAATGAGCTCGCGCAACATTCAAA	3912	5581	TGCACGCGCTCCCGCGCGCAAAATTTTCTAGGCGCTGTGGCGGGTGGTGTCTGAGAG	5640
Db	4501	GAGTGCCTCTCACACCTCCCTTACATCGAACAGGAAATGAGCTCGCGCAACATTCAAA	4560	4993	TACGTGGAGGTTACCGGGTGGGGGATTTCCATCTACGTGAGCGGCATGACCACTGACAC	5052
QY	3913	CAGAAGCAATCGGGTTGTCTCAAAACAGCCACCAAGCAAGCGAGGCTGTCTCCCGTG	3972	5641	TACGTGGAGGTTACCGGGTGGGGGATTTCCATCTACGTGAGCGGCATGACCACTGACAC	5700
Db	4561	CAGAAGCAATCGGGTTGTCTCAAAACAGCCACCAAGCAAGCGAGGCTGTCTCCCGTG	4620	5053	GTAAAGTCCCGGTGTCTAGGTTCCGGCGCCCGAATTTCTTACAGAAATGGATGGGGTGGG	5112
QY	3973	GTGGAATCCAAAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATGTGAAATTCATC	4032	5701	GTAAAGTCCCGGTGTCTAGGTTCCGGCGCCCGAATTTCTTACAGAAATGGATGGGGTGGG	5760
Db	4621	GTGGAATCCAAAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATGTGAAATTCATC	4680	5113	TTGCACAGGTACGCTCCAGCGTGCACACCCCTCTTACGGGAGGAGGTCACTTCTGTCTC	5172
QY	4033	AGCGGATACAAATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCCCGCGATAGCATCA	4092	5761	TTGCACAGGTACGCTCCAGCGTGCACACCCCTCTTACGGGAGGAGGTCACTTCTGTCTC	5820
Db	4681	AGCGGATACAAATTTAGCAGGCTTGTCCACTCTGCTGCGCAACCCCGCGATAGCATCA	4740	5173	GGGCTCAATCAATACCTGGTTGGGTTCAGCTTCCATTCGAGCGCCGAAACCGGACGTAGCA	5232
QY	4093	CTGATGGCAATTCACAGCTCTATCACAGCCCGCTCACACCCCAATACCCCTCTGTCT	4152	5821	GGGCTCAATCAATACCTGGTTGGGTTCAGCTTCCATTCGAGCGCCGAAACCGGACGTAGCA	5880
Db	4741	CTGATGGCAATTCACAGCTCTATCACAGCCCGCTCACACCCCAATACCCCTCTGTCT	4800	5233	GTGCTCATCTTCATGCTCACGACCCCTCCACATTTACGGGAGGAGCGCTAAGCGTAGG	5292
QY	4153	AACATCTGGGGGATGGGTGGCGCCGCAACTTCTCTCCAGCGCTCTTCTGCTTTC	4212	5881	GTGCTCATCTTCATGCTCACGACCCCTCCACATTTACGGGAGGAGCGCTAAGCGTAGG	5940
Db	4801	AACATCTGGGGGATGGGTGGCGCCGCAACTTCTCTCCAGCGCTCTTCTGCTTTC	4860	5293	CTGGCCAGGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGCT	5352
QY	4213	GTAGGCGCGGATCGCTGGAGCGGCTGTGCGAGCATAGGCTTTGGGAAGGTGTGTG	4272	5941	CTGGCCAGGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGCT	6000
Db	4861	GTAGGCGCGGATCGCTGGAGCGGCTGTGCGAGCATAGGCTTTGGGAAGGTGTGTG	4920	5353	TCCTTTGAAGGCAACATGCACTACCCGCTCATGCTCCCGGAGCGCTCATCAGGCGC	5412
QY	4273	GATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTGTGCGCTTTAAGGTCATG	4332	6001	TCCTTTGAAGGCAACATGCACTACCCGCTCATGCTCCCGGAGCGCTCATCAGGCGC	6060
Db	4921	GATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTGTGCGCTTTAAGGTCATG	4980	5413	AACTCTCTGTGGCGGAGGATGGCGGAAATCATCCCGGCTGGAGTCAGAAATAAG	5472
QY	4333	AGCGGCGAGATGCCCTCACCGAGGACCTGGTTAACTCTCTCTCTCTCTCTCTCT	4392	6061	AACTCTCTGTGGCGGAGGATGGCGGAAATCATCCCGGCTGGAGTCAGAAATAAG	6120
Db	4981	AGCGGCGAGATGCCCTCACCGAGGACCTGGTTAACTCTCTCTCTCTCTCTCTCT	5040	5473	GTAGTAATTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGATGAGAGGAGTATCTCC	5532
QY	4393	GGCGCCCTAGTCTCGGGGTCTGTGCGCAGCGATCTGCTGCGGACGCTGGGCGCCAGGG	4452			

Db	6121	GTAGTAAATTTTGGACTCTTTTCAGCGCGCTCCAAGCGGAGGAGGATGAGAGGGAGTATCC	6181
Qy	5533	GTTCGGGGGAGATCTCTGGAGGTCCAGAAATTCCTTCGACGATGCCCATATGGCA	5592
Db	6181	GTTCGGGGGAGATCTCTGGAGGTCCAGAAATTCCTTCGACGATGCCCATATGGCA	6240
Qy	5593	GCCTCGGATTAACAACCTTCACTGTGTAGAGTCTCTGGAAGGACCGGACTACGTCCCTCCA	5652
Db	6241	CGCCCGGATTAACAACCTTCACTGTGTAGAGTCTCTGGAAGGACCGGACTACGTCCCTCCA	6300
Qy	5653	GTGTGTACACGGGTGTCATTGCGCGCTGCAAGGCCCTTCGATACCACTCCACGGAGG	5712
Db	6301	GTGTGTACACGGGTGTCATTGCGCGCTGCAAGGCCCTTCGATACCACTCCACGGAGG	6360
Qy	5713	AAGAGGACGGTTGTCTCTGCAGAACTTACCGTGTCTTCTGCTTCGGCGAGTTCGGCACA	5772
Db	6361	AAGAGGACGGTTGTCTCTGCAGAACTTACCGTGTCTTCTGCTTCGGCGAGTTCGGCACA	6420
Qy	5773	AAGACTTTCGCGAGTTCGGAATTCGTCGCGCTGCAAGCGGCACGCGACCGCGCTCTCT	5832
Db	6421	AAGACTTTCGCGAGTTCGGAATTCGTCGCGCGCTGCAAGCGGCACGCGACCGCGCTCTCT	6480
Qy	5833	GACCAGCCCTCCGACGACGGCGACGCGGATCCGACGTTGAGTGTCTCTCCATGCGCC	5892
Db	6481	GACCAGCCCTCCGACGACGGCGACGCGGATCCGACGTTGAGTGTCTCTCCATGCGCC	6540
Qy	5893	CCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGCGACGGGTCTTGCTTACCGTAAGC	5952
Db	6541	CCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGCGACGGGTCTTGCTTACCGTAAGC	6600
Qy	5953	GAGGAGCTAGTGAGGAGTCTGTGTGTCTGATGTCCTACATGACGACGGCGCCCTG	6012
Db	6601	GAGGAGCTAGTGAGGAGTCTGTGTGTCTGATGTCCTACATGACGACGGCGCCCTG	6660
Qy	6013	ATCACGCCATCGCTCGGAGGAACCAAGCTGCCCATCAATGCACTGAGCAACTCTTTTG	6072
Db	6661	ATCACGCCATCGCTCGGAGGAACCAAGCTGCCCATCAATGCACTGAGCAACTCTTTTG	6720
Qy	6073	CTCGGTCAACACAATTGGTCTATGTCTACAACATCTCGACGCAAGCCTCGGCGAAG	6132
Db	6721	CTCGGTCAACACAATTGGTCTATGTCTACAACATCTCGACGCAAGCCTCGGCGAAG	6780
Qy	6133	AAGGTCACTTTGACAGATGCGAGGTCTCGACGACCACTACCGGACGTGCTCAAGGAG	6192
Db	6781	AAGGTCACTTTGACAGATGCGAGGTCTCGACGACCACTACCGGACGTGCTCAAGGAG	6840
Qy	6193	ATGAAGCGCAAGCGCTCCAGATTAGGCTTAACTTCTATCCGTGGAGGAAGCTGTAAAG	6252
Db	6841	ATGAAGCGCAAGCGCTCCAGATTAGGCTTAACTTCTATCCGTGGAGGAAGCTGTAAAG	6900
Qy	6253	CTGAGCCGCCCAATTCGCGCAGATCTAAATTTGGTCTATGGGGCAAGGACGTCGCGAAC	6312
Db	6901	CTGAGCCGCCCAATTCGCGCAGATCTAAATTTGGTCTATGGGGCAAGGACGTCGCGAAC	6960
Qy	6313	CTATCCAGCAAGCCGTTAACCACTCCGCTCGGTGGGAAGCACTTGCTGGGAAGCACT	6372
Db	6961	CTATCCAGCAAGCCGTTAACCACTCCGCTCGGTGGGAAGCACTTGCTGGGAAGCACT	7020
Qy	6373	GAGACCAATTTGACACCACTCATGGCAAAATAGGTTTTCTCGCTTCAACCAAGAG	6432
Db	7021	GAGACCAATTTGACACCACTCATGGCAAAATAGGTTTTCTCGCTTCAACCAAGAG	7080
Qy	6433	AAGGGGGCGCAAGCCAGCTCGCTTATTCGATTCGAGATTGGGGTTCGTGTGTC	6492
Db	7081	AAGGGGGCGCAAGCCAGCTCGCTTATTCGATTCGAGATTGGGGTTCGTGTGTC	7140
Qy	6493	GAGAAATGGCCCTTTACGATGTGTTCCACCTCCCTCAGGCCGTGATGGCTCTTCA	6552
Db	7141	GAGAAATGGCCCTTTACGATGTGTTCCACCTCCCTCAGGCCGTGATGGCTCTTCA	7200
Qy	6553	TACGGATTCCAATACTCTCTCGACAGCGGTGCGAGTTCTCGTGAATGCTGGAAAGCG	6612
Db	7201	TACGGATTCCAATACTCTCTCGACAGCGGTGCGAGTTCTCGTGAATGCTGGAAAGCG	7260

QY	6613	AAGAAATGCCCTATATGGCTTCGCAATATGACACCCGCTGTTTGTACTCAACGGTCACTGAG	6672
Db	7261	AAGAAATGCCCTATATGGCTTCGCAATATGACACCCGCTGTTTGTACTCAACGGTCACTGAG	7320
QY	6673	AATGACATCCGTGTTGAGAGTCAATCTACAAATGTTGTGACTTGGCCCCCGAAGCCAGA	6732
Db	7321	AATGACATCCGTGTTGAGAGTCAATCTACAAATGTTGTGACTTGGCCCCCGAAGCCAGA	7380
QY	6733	CAGGCCATAAGTTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTGACTTAATTTCTAAA	6792
Db	7381	CAGGCCATAAGTTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTGACTTAATTTCTAAA	7440
QY	6793	GGGAGAACTCGCGCTATCGCCGCTGCGCGAGCGGTGACTGACCAAGCTGCGGT	6852
Db	7441	GGGAGAACTCGCGCTATCGCCGCTGCGCGAGCGGTGACTGACCAAGCTGCGGT	7500
QY	6853	AATACCCCTCACATGTTACTTTGAAGCCCGCTGCGGCCCTGTGAGCTGCGAAGCTCCAGGAC	6912
Db	7501	AATACCCCTCACATGTTACTTTGAAGCCCGCTGCGGCCCTGTGAGCTGCGAAGCTCCAGGAC	7560
QY	6913	TGCACGATGCTCGTATGCGGAGAGACCTTGTGCTTATCTGTGAAAGCGCGGGGACCCAA	6972
Db	7561	TGCACGATGCTCGTATGCGGAGAGACCTTGTGCTTATCTGTGAAAGCGCGGGGACCCAA	7620
QY	6973	GAGGACGAGCGAGCCCTACGGGCGCTTCAAGCGAGGCTATGACTAGATATCTGCCCCCCT	7032
Db	7621	GAGGACGAGCGAGCCCTACGGGCGCTTCAAGCGAGGCTATGACTAGATATCTGCCCCCCT	7680
QY	7033	GGGGACCCGCCCAAAACGAGNATAGACTTGGAGTTGATATAATCATGCTCTCTCAATGTG	7092
Db	7681	GGGGACCCGCCCAAAACGAGNATAGACTTGGAGTTGATATAATCATGCTCTCTCAATGTG	7740
QY	7093	TCAGTCCGCGACGATGCATCTGCCAAAAGGCTGACTATCTCAACCGTGACCCACACC	7152
Db	7741	TCAGTCCGCGACGATGCATCTGCCAAAAGGCTGACTATCTCAACCGTGACCCACACC	7800
QY	7153	CCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAGGC	7212
Db	7801	CCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAGGC	7860
QY	7213	AACATCATCATGATGCGGCCCACTTGTGGGCAAGGATGATCCTGATGACTCATTTCTTC	7272
Db	7861	AACATCATCATGATGCGGCCCACTTGTGGGCAAGGATGATCCTGATGACTCATTTCTTC	7920
QY	7273	TCCATCCTTCTAGCTCAGGAAACAATTGAAAAGCCCTAGATTGTGAGATCTACGGGGCC	7332
Db	7921	TCCATCCTTCTAGCTCAGGAAACAATTGAAAAGCCCTAGATTGTGAGATCTACGGGGCC	7980
QY	7333	TGTTACTCGATGAGCCACTTGACCTACCTCAGATCAITTCACAGACTCCATGGCCCTTAGC	7392
Db	7981	TGTTACTCGATGAGCCACTTGACCTACCTCAGATCAITTCACAGACTCCATGGCCCTTAGC	8040
QY	7393	GCATTTTCACTCCATAGTTACTCTCCAGTGAGATCAATAGGGTGGCTTCATGCTCAGG	7452
Db	8041	GCATTTTCACTCCATAGTTACTCTCCAGTGAGATCAATAGGGTGGCTTCATGCTCAGG	8100
QY	7453	AAACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGCCAGAGTGTCCGCGCTAGG	7512
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QY	7513	CTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTTCAACTGGGCACTA	7572
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QY	7573	AGGACCAAGCTCAAACTCACTCCAAATCCCGCTGCTCCCAAGTTGGATTTATCCAGCTGG	7632
Db	8221	AGGACCAAGCTCAAACTCACTCCAAATCCCGCTGCTCCCAAGTTGGATTTATCCAGCTGG	8280
QY	7633	TTCGTTGCTGTTACAGCGGGGAGACATATATCACAGCTGTCTCTGTCCCGACCCCGC	7692
Db	8281	TTCGTTGCTGTTACAGCGGGGAGACATATATCACAGCTGTCTCTGTCCCGACCCCGC	8340

7693 TGGTTCATGCGGCTACTCTACTTTCTAGGGTAGGCATCTACTATCCCAAC 7752
 Db 8341 TGGTTCATGCGGCTACTCTACTTTCTAGGGTAGGCATCTACTATCCCAAC 8400
 Qy 7753 CGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTTTCCCTTTT 7812
 Db 8401 CGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTTTCCCTTTT 8460
 Qy 7813 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7872
 Db 8461 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 8520
 Qy 7873 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7932
 Db 8521 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 8580
 Qy 7933 GTCGTCGACCGCTTGACTGCAGAGAGTCTGATCTGCGCTCTCTGCAGATCAAGT 7989
 Db 8581 GTCGTCGACCGCTTGACTGCAGAGAGTCTGATCTGCGCTCTCTGCAGATCAAGT 8637

RESULT 7

US-09-539-601-13
 ; Sequence 13, Application US/09539601C
 ; Patent No. 6630343
 ; GENERAL INFORMATION:
 ; APPLICANT: Bartenschlager, Ralf FW
 ; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
 ; FILE REFERENCE: all sequences
 ; CURRENT APPLICATION NUMBER: US/09/539,601C
 ; CURRENT FILING DATE: 2001-08-30
 ; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
 ; EARLIER FILING DATE: 1999-04-03
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 8649
 ; TYPE: DNA
 ; ORGANISM: Hepatitis C virus
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: (1)...(341)
 ; OTHER INFORMATION: construct 1389/NS2-3'/wt
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (342)..(1193)
 ; OTHER INFORMATION: hepatitis c virus core-neomycin phosphotransferase
 ; OTHER INFORMATION: fusion protein
 ; FEATURE:
 ; NAME/KEY: RBS
 ; LOCATION: (1202)..(1812)
 ; OTHER INFORMATION: internal ribosome entry site of
 ; OTHER INFORMATION: encephalomyocarditis virus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1813)..(8418)
 ; OTHER INFORMATION: hepatitis C virus NS2 - 5B
 ; FEATURE:
 ; NAME/KEY: 3'UTR
 ; LOCATION: (8419)..(8649)
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Lohmann, Volker
 ; AUTHORS: Krner, Frank
 ; AUTHORS: Koch, Jan-Oliver
 ; AUTHORS: Herian, Ulrike
 ; AUTHORS: Theilmann, Lorenz
 ; AUTHORS: Bartenschlager, Ralf
 ; TITLE: Replication of subgenomic hepatitis c virus RNAs in a
 ; TITLE: hepatoma cell line
 ; JOURNAL: Science
 ; VOLUME: 285
 ; PAGES: 110-113
 ; DATE: 1999-07-02

US-09-539-601-13
 Query Match 91.5%; Score 7309; DB 4; Length 8649;
 Best Local Similarity 92.4%; Pred. No. 0;
 Matches 7989; Conservative 0; Mismatches 0; Indels 660; Gaps 2;
 Qy 1 GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60
 Db 1 GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60
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 Db 61 TCTTCACGACAGAAAGCGTCTAGCCATGCGTGTAGTATGAGTGTCTGCGAGCTCCAGGAC 120
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 Db 121 CCCCCCTCCGCGAGAGCCATAGTGTCTGCGGAAACCGGTGAGTACACCGGAATGCGCAG 180
 Qy 181 GACGACCGGGTCTTTCTTGGATCAACCGGCTCAATGCTGAGATTTGGGGTGCCTCC 240
 Db 181 GACGACCGGGTCTTTCTTGGATCAACCGGCTCAATGCTGAGATTTGGGGTGCCTCC 240
 Qy 241 GCGAGACTCTAGCCGAGTAGTGTGGTTCGCGAAAGGCTTGTGTACTCTGCTGTAGG 300
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 Qy 301 GTGCTTGGAGTGCCCGGGAGGTCTCTGTAGACCGGTGACCATGACAGATCTCTAAAC 360
 Db 301 GTGCTTGGAGTGCCCGGGAGGTCTCTGTAGACCGGTGACCATGACAGATCTCTAAAC 360
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 Db 361 CTCAAAAGAAAAACCAAA-----GGGGCGCCCATGATTGAACAGATGGATTGC 420
 Qy 409 ACCGAGTTCTCCGGCGCGTGGTGGAGAGGTATTTCGGCTATGATCGGCGCAACAGA 468
 Db 421 ACGGAGTTCTCCGGCGCGTGGTGGAGAGGTATTTCGGCTATGATCGGCGCAACAGA 480
 Qy 469 CAATCGGCTCTGTATGCGCGCGTGTTCGGTGTGAGCGAGGGCGCGGTTCTTT 528
 Db 481 CAATCGGCTCTGTATGCGCGCGTGTTCGGTGTGAGCGAGGGCGCGGTTCTTT 540
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 Db 541 TTGTCAAGACCGACTGTCCGTCCTGATGAATGAGTGCAGGACGAGCGCGGCTAT 600
 Qy 589 CGTGGCTGGCCACGACGGGGGTTCTTTCGCGAGCTGTGCTCGACGTTGTCTCAAGCGG 648
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 Qy 709 CTCCTGCGGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGATACGCTGTGATC 768
 Db 721 CTCCTGCGGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGATACGCTGTGATC 780
 Qy 769 CGGCTACCTGCCCATTTGACACCAAGCAACATCGCATCGAGCGACGATCTCTCGGA 828
 Db 781 CGGCTACCTGCCCATTTGACACCAAGCAACATCGCATCGAGCGACGATCTCTCGGA 840
 Qy 829 TGGAGCGGCTCTTGTTCGATCAGGATGATCGGAGAGATCGAGGATCGGGCTCGCGCCAG 888
 Db 841 TGGAGCGGCTCTTGTTCGATCAGGATGATCGGAGAGATCGAGGATCGGGCTCGCGCCAG 900
 Qy 889 CCGAACTGTTGCGCAGGCTCAAGCGCGCATGCGCGAGGATCTCGTGTGACCC 948
 Db 901 CCGAACTGTTGCGCAGGCTCAAGCGCGCATGCGCGAGGATCTCGTGTGACCC 960
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 Db 961 ATGGCGATGCGCTTTCGCGAATATATGTTGGAATAATGGCGCTTTTCTGTGATTCATCG 1020

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1021 ACTGTGCGCGCTGGGTGTCGGCGACCGCTATCAGGACATAGCGTTGGCTACCGTGATA 1080
1069 TTGCTGAAGAGCTTGGCGGGAATGGGCTCAGCGCTTCTCGTGTCTTACGGTATCGCG 1128
1081 TTGCTGAAGAGCTTGGCGGGAATGGGCTCAGCGCTTCTCGTGTCTTACGGTATCGCG 1140
1129 CTCGGATTCGCGAGCGATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAA 1188
1141 CTCGGATTCGCGAGCGATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAA 1200
1189 CAGACACAACGCTTTCCTCTAGCGGATCAATTCGCGCTTCTCGCTCCCCCCCCCT 1248
1201 CAGACACAACGCTTTCCTCTAGCGGATCAATTCGCGCTTCTCGCTCCCCCCCCCT 1260
1249 AAGCTTACTGGCGAAGCGCTTGGATAAGGCGGTGTCGGTTCTCTATATGTTATT 1308
1261 AAGCTTACTGGCGAAGCGCTTGGATAAGGCGGTGTCGGTTCTCTATATGTTATT 1320
1309 TCCACATATTGCGCTTCTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTTCTTG 1368
1321 TCCACATATTGCGCTTCTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTTCTTG 1380
1369 ACGAGCATTCCTAGGGCTTCTTCCCTCTCGCAAGGATGCAAGGTCTGTGATGTC 1428
1381 ACGAGCATTCCTAGGGCTTCTTCCCTCTCGCAAGGATGCAAGGTCTGTGATGTC 1440
1429 GTGAAGAGCAGTTCCTCTGGAAGCTTCTTGAAGACAACACCTGTGTAGCGACCTT 1488
1441 GTGAAGAGCAGTTCCTCTGGAAGCTTCTTGAAGACAACACCTGTGTAGCGACCTT 1500
1489 TCGAGGACCGGAACCCCGCTCTGGGACAGGTGCTCTGGGCAAAAGCCAGTGT 1548
1501 TCGAGGACCGGAACCCCGCTCTGGGACAGGTGCTCTGGGCAAAAGCCAGTGT 1560
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1561 TAAGATACACCTGCAAGGCGGCAACCCAGTGCAGGTGTGAGTTGATAGTTGT 1620
1609 GAAAGGTCAATAGGCTCTCTCAAGGCTATTCAAGAGGGCTGAAGGATGCCAGAAG 1668
1621 GAAAGGTCAATAGGCTCTCTCAAGGCTATTCAAGAGGGCTGAAGGATGCCAGAAG 1680
1669 GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGCATGCTTTACATGTTTAT 1728
1681 GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGCATGCTTTACATGTTTAT 1740
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2281 GACCTTGGGTGGCAGTGTGAGCCCGTGTCTCTGATATGGAGACCAAGTTTATCACC 2340
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2341 TGGGGGGCAGACACCGCGGCTGTGGGGACATCATTTGGGCTTGCCTCTCGGCCG 2400
1804 ----- 1803
2401 AGGGGAGGAGATACATCTGGGACCGGCAGACAGCTTGAAGGCGAGGGTGGCGACTC 2460
1804 ---GCGCCTATTACCGCTTACTCCCAACAGACGCGAGGCTACTTTGGCTGCATCATCACT 1860
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2521 AGCTTCACAGCGCGGACAGAAACAGGTCCGAGGGGAGGTCCAAAGTGTCTCCACGCA 2580
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2881 GGCGGCTCACTGTCTCTCGCCCTCGGGGCGCTTCTGAGGATCTTTCGGGCTGCGGTGC 2340
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2941 ACCGAGGGGTTGCGAAGCGGTGAGTCTTGTACCCGCTAGGCTATGAAACCACTATG 3000
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3061 GCGCATCTACAGCGCCCTTACTGAGCGGAGCTTTCGGGCTGCGGTGCGGTATGCA 3120
2461 GCGCAAGGTTAAGTGTCTTCTGAAACCGCTCGGCGGCGGCGGCGGCGGCTAGGTTTCGG 2520
3121 GCGCAAGGTTAAGTGTCTTCTGAAACCGCTCGGCGGCGGCGGCGGCGGCTAGGTTTCGG 3180
2521 GCGTATGTTCTAAGGCACATGGTATCGACCTTAACATCAAGAACCGGGGTGAAGGACATC 2580

Tue Nov 2 14:02:16 2004

Db	3181	GCATATATGCTAAGGCACATGGTATCGACCTAATCAATCAAGAACCGGGGTAAAGACCATC	3240
QY	2581	ACACGGGTGCCCCCATCAGCTACTCTACCTATGCAAGTATTTCTTGCCGACGGTGTTC	2640
Db	3241	ACACGGGTGCCCCCATCAGCTACTCTACCTATGCAAGTATTTCTTGCCGACGGTGTTC	3300
QY	2641	TCTGGGGGCGCTATGACATCATATATGTGATGAGTGCCTCACTGACTCGACCACT	2700
Db	3301	TCTGGGGGCGCTATGACATCATATATGTGATGAGTGCCTCACTGACTCGACCACT	3360
QY	2701	ATCTGGGATCGGCACAGTCTCTGACCAAGCGGAGAGCGCTGAGCGCACTCTGCTG	2760
Db	3361	ATCTGGGATCGGCACAGTCTCTGACCAAGCGGAGAGCGCTGAGCGCACTCTGCTG	3420
QY	2761	CTGCGCACCGCTACCGCTCTCGGATCGGTCAACGAGGAGAGCGCTGAGCGCACTCTGCTG	2820
Db	3421	CTGCGCACCGCTACCGCTCTCGGATCGGTCAACGAGGAGAGCGCTGAGCGCACTCTGCTG	3480
QY	2821	GCTCTGTCAGACACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGCCATC	2880
Db	3481	GCTCTGTCAGACACTGGAGAAATCCCTTTTATGGCAAGGCAATCCCATCGAGCCATC	3540
QY	2881	AAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAGAAATGTGATGAGCTCGCGCG	2940
Db	3541	AAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAGAAATGTGATGAGCTCGCGCG	3600
QY	2941	AAGCTGTCGGCTCGGACCTCAATGTGTAGCATATTTACCGGGGCTTTGATGATCGTC	3000
Db	3601	AAGCTGTCGGCTCGGACCTCAATGTGTAGCATATTTACCGGGGCTTTGATGATCGTC	3660
QY	3001	ATACCAACTAGCGAGACGTCATGTCTGTAGCAATTCGAAGAGGCAATGATGAGCTTTACC	3060
Db	3661	ATACCAACTAGCGAGACGTCATGTCTGTAGCAATTCGAAGAGGCAATGATGAGCTTTACC	3720
QY	3061	GGGATTTGAGCTCAGTGATCGATGCAATATGTCACCCAGACAGTGCATCTCAGC	3120
Db	3721	GGGATTTGAGCTCAGTGATCGATGCAATATGTCACCCAGACAGTGCATCTCAGC	3780
QY	3121	CTGACCCGACCTTACCATTGAGACGACGCGTGGCCACAGACGCGGTGTACGCTCG	3180
Db	3781	CTGACCCGACCTTACCATTGAGACGACGCGTGGCCACAGACGCGGTGTACGCTCG	3840
QY	3181	CAGCGCGGAGGACGACTGTGAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA	3240
Db	3841	CAGCGCGGAGGACGACTGTGAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA	3900
QY	3241	GAAAGGCTTGGGCACTGTCGATTCCTCGGTCTGTGCGAGTGTATGACGCGGGCTGT	3300
Db	3901	GAAAGGCTTGGGCACTGTCGATTCCTCGGTCTGTGCGAGTGTATGACGCGGGCTGT	3960
QY	3301	GCTTGTAGAGCTCAGCGCCCGGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA	3360
Db	3961	GCTTGTAGAGCTCAGCGCCCGGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA	4020
QY	3361	CCAGGGTTCGGCTGTGCGAGGACATCTGGAGTCTGGAGAGCGCTTTACAGGCCCTC	4080
Db	4021	CCAGGGTTCGGCTGTGCGAGGACATCTGGAGTCTGGAGAGCGCTTTACAGGCCCTC	4140
QY	3421	ACCCATAGACGCCATTTCTGTCCAGACTTAAGCAGCAGGAGACAACTTCCCTTAC	3480
Db	4081	ACCCATAGACGCCATTTCTGTCCAGACTTAAGCAGCAGGAGACAACTTCCCTTAC	4140
QY	3481	CTGGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCATCTGTGGAC	3540
Db	4141	CTGGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCATCTGTGGAC	4200
QY	3541	CAAAATGGAGTGTCTCATACGGCTAAAGCTTACGCTGACCGGGCCAGCGCCCTGCTG	3600
Db	4201	CAAAATGGAGTGTCTCATACGGCTAAAGCTTACGCTGACCGGGCCAGCGCCCTGCTG	4260
QY	3601	TATAGGCTGGAGCGGTTCAAAAGCAGGTTACTACCAACACACCCCAATCAATC	3660
Db	4261	TATAGGCTGGAGCGGTTCAAAAGCAGGTTACTACCAACACACCCCAATCAATC	4320
QY	3661	ATGCACTGATGTGGCTGACCTGAGAGGTCTGACAGCACTGGTCTGCTGAGGGGA	3720
Db	4321	ATGCACTGATGTGGCTGACCTGAGAGGTCTGACAGCACTGGTCTGCTGAGGGGA	4380
QY	3721	GTCTTAGAGCTGTGGCGCGCTATGCTGACCAACAGCAGCGTGTCTATTTGGGCGAGG	3780
Db	4381	GTCTTAGAGCTGTGGCGCGCTATGCTGACCAACAGCAGCGTGTCTATTTGGGCGAGG	4440
QY	3781	ATCATCTTGTTCGGAAAGCGGCTCATTTCCCGACAGGAAAGTCTTTACCGGAGTTC	3840
Db	4441	ATCATCTTGTTCGGAAAGCGGCTCATTTCCCGACAGGAAAGTCTTTACCGGAGTTC	4500
QY	3841	GATGAGATGGAAGAGTGGCGCTCACAACCTCTTACATCGAACAGGAAATGAGCTCGCC	3900
Db	4501	GATGAGATGGAAGAGTGGCGCTCACAACCTCTTACATCGAACAGGAAATGAGCTCGCC	4560
QY	3901	GAAACATTTCAACAGAGGCAATCGGGTGTGCAACAGCAGCCACCAAGCAAGCGGAGCT	3960
Db	4561	GAAACATTTCAACAGAGGCAATCGGGTGTGCAACAGCAGCCACCAAGCAAGCGGAGCT	4620
QY	3961	GCTGCTCCGCTGGTGAATCCAAAGTGGCGGACCTCGAAAGCTTCTGGGGGAGCATATG	4020
Db	4621	GCTGCTCCGCTGGTGAATCCAAAGTGGCGGACCTCGAAAGCTTCTGGGGGAGCATATG	4680
QY	4021	TGGAAATTTCAACAGCGGATACAAATATTTAGCAGGCTTCTGCACTCTGCTGCAACCCC	4080
Db	4681	TGGAAATTTCAACAGCGGATACAAATATTTAGCAGGCTTCTGCACTCTGCTGCAACCCC	4740
QY	4081	GCGATGATCATGATGAGGCAATTCACAGCTCTATCACAGCCGCTTCCACCCCAACAT	4140
Db	4741	GCGATGATCATGATGAGGCAATTCACAGCTCTATCACAGCCGCTTCCACCCCAACAT	4800
QY	4141	ACCTCTCTGTTTAACTCTCTGGGGGATGGTGGCCGCCCAACTTCTCTCCAGCGCT	4200
Db	4801	ACCTCTCTGTTTAACTCTCTGGGGGATGGTGGCCGCCCAACTTCTCTCCAGCGCT	4860
QY	4201	GCTTCTGCTTTCGAGCGCGCGCATGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4260
Db	4861	GCTTCTGCTTTCGAGCGCGCGCATGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG	4920
QY	4261	AAGTGTCTGTGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGCGCTCTGTGCGC	4320
Db	4921	AAGTGTCTGTGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGCGCTCTGTGCGC	4980
QY	4321	TTTAAAGTCTAGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTTCTCTCTGCT	5040
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QY	4381	ATCTCTCTCCCTGGCGCTTAGTCTGGGTCTGTCGAGCGGATGCTGCTGGGCAAC	4440
Db	5041	ATCTCTCTCCCTGGCGCTTAGTCTGGGTCTGTCGAGCGGATGCTGCTGGGCAAC	5100
QY	4441	GTGGGCGGAGGAGGCGGCTGTGAGTGGATGAACCGGCTGATAGCGTTCGCTGGCGG	4500
Db	5101	GTGGGCGGAGGAGGCGGCTGTGAGTGGATGAACCGGCTGATAGCGTTCGCTGGCGG	5160
QY	4501	GCTTAAACAGCTCTCCCGCCACGCACTATGTGCTGAGAGCGGCTGTCAGCGTGTCACT	4560
Db	5161	GCTTAAACAGCTCTCCCGCCACGCACTATGTGCTGAGAGCGGCTGTCAGCGTGTCACT	5220
QY	4561	CAGATCTCTTAGTCTTACCATCTAGCTCTGCTGAGAGGCTTCCACAGTGGATCAAC	4620
Db	5221	CAGATCTCTTAGTCTTACCATCTAGCTCTGCTGAGAGGCTTCCACAGTGGATCAAC	5280
QY	4621	GAGGATCTCTCAGCGCATGCTCCGGCTGTGGCTTAAGAGATTTTGGGATTTGGATGTC	4680
Db	5281	GAGGATCTCTCAGCGCATGCTCCGGCTGTGGCTTAAGAGATTTTGGGATTTGGATGTC	5340
QY	4681	ACGGTGTGATGATTTCAAGACCTGGCTCCAGTCCAGCTCTGCGCGGATTTCCCGGA	4740
Db	5341	ACGGTGTGATGATTTCAAGACCTGGCTCCAGTCCAGCTCTGCGCGGATTTCCCGGA	5400

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7381 CCGGAGCGGAGGAGGAGTCAATGAGTCTGCTGCAAGCGGCTTTTACATCGGCGGCCCTG 7440
6781 ACTAATTTTAAAGGCGGAGAACTCGGCTATCCGCTGCGCGGAGCGGCTTACTGAG 6840
7441 ACTAATTTTAAAGGCGGAGAACTCGGCTATCCGCTGCGCGGAGCGGCTTACTGAG 7500
6841 ACCAGTCCGGTAAATACCTTCAATGTTTACTTGAAGCGGCTGCGGCGGCTGAGTGG 6900
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6901 AAGCTCCAGGACTGCAAGTCTGCTGCGGAGGAGGAGTCTGCTGTTGTTGAAAGC 6960

Db 8641 AGATCAAGT 8649

RESULT 8
 US-10-029-907-1
 ; Sequence 1, Application US/10029907
 ; Patent No. 6706874
 ; GENERAL INFORMATION:
 ; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
 ; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
 ; TITLE OF INVENTION: HEPATITIS C VIRUS
 ; FILE REFERENCE: 13/083
 ; CURRENT APPLICATION NUMBER: US/10/029,907
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 60/257,857
 ; PRIOR FILING DATE: 2000-12-22
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 8639
 ; TYPE: DNA
 ; ORGANISM: HCV
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1803)....(8408)
 US-10-029-907-1

Query Match 91.0%; Score 7273.8; DB 4; Length 8639;
 Best Local Similarity 92.2%; Pred. No. 0;
 Matches 7976; Conservative 0; Mismatches 2; Indels 671; Gaps 3;

QY	1	GCACGCCCGGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAAC	CTG	60
Db	2	GCACGCCCGGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAAC	CTG	61
QY	61	TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTC	CAGAC	120
Db	62	TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTC	CAGAC	121
QY	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGGGAACCGGTGAGTACACGGAAATG	CCAG	180
Db	122	CCCCCTCCCGGAGAGCCATAGTGGTCTGGGAACCGGTGAGTACACGGAAATG	CCAG	181
QY	181	GAGCACCGGTCCTTTCTTGATCAACCGCTCAATGCTCGAGATTTGGCGGTG	CCCC	240
Db	182	GAGCACCGGTCCTTTCTTGATCAACCGCTCAATGCTCGAGATTTGGCGGTG	CCCC	241
QY	241	GCAGAGACTGTAGCCGAGTAGTGTGGGTGCGGAAAGCGCTTGTGGTACTG	CTCATAGG	300
Db	242	GCAGAGACTGTAGCCGAGTAGTGTGGGTGCGGAAAGCGCTTGTGGTACTG	CTCATAGG	301
QY	301	GTGCTTGCAGAGTCCCGGAGAGTCTCGTAGACCGTGACCATGACGCAATC	CTAAAC	360
Db	302	GTGCTTGCAGAGTCCCGGAGAGTCTCGTAGACCGTGACCATGACGCAATC	CTAAAC	361
QY	361	CTCAAGAAAAACAAGGCGCGCATGATTGAACAAGATGGATTGCACGAGTTCT	C	420
Db	362	CTCAAGAAAAACAAGGCGCGCATGATTGAACAAGATGGATTGCACGAGTTCT	C	421
QY	421	CGGCGGCTTGGGTGGAGAGCTATTGCGGTATGACTGGGCAACAACAGCAAT	CGGCTGCT	480
Db	422	CGGCGGCTTGGGTGGAGAGCTATTGCGGTATGACTGGGCAACAACAGCAAT	CGGCTGCT	481
QY	481	CTGATGCGCGGTGTTCCGGCTGTACGCGCAGGCGCGCGGTCTCTTTTGTCA	AGACCG	540
Db	482	CTGATGCGCGGTGTTCCGGCTGTACGCGCAGGCGCGCGGTCTCTTTTGTCA	AGACCG	541
QY	541	ACCTGTCCGCTGCGCTCAATGAATGAACTGCAGGACGAGGACGCGGCTAT	CGTGCTGGCCA	600
Db	542	ACCTGTCCGCTGCGCTCAATGAATGAACTGCAGGACGAGGACGCGGCTAT	CGTGCTGGCCA	601
QY	601	CGACGGCGGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAACGCGGAGG	ACTGCG	660

7561	Db		AAGCTCAGGACTGCAAGATGCTGTATTCGGAGACGACCTTGCTTATCTGTGAAGC	7620
6961	Qy		GCGGGACCCAAAGAGGACGAGCGAGCCCTACGGGCTTTCAGGAGGCTATGACTAGATAC	7020
7621	Db		GCGGGACCCAAAGAGGACGAGCGAGCCCTACGGGCTTTCAGGAGGCTATGACTAGATAC	7680
7021	Qy		TCTGCCCCCTCGGGGACCCGGCCAAACGAGAAATAGGACTTCGGAGTTGATACATCATCAG	7080
7681	Db		TCTGCCCCCTCGGGGACCCGGCCAAACGAGAAATAGGACTTCGGAGTTGATACATCATCAG	7740
7081	Qy		TCTTCAATGTGTAGTTCGCGCAGCATGCTGGCAAAAGGCTGTACTATCTCACCGGT	7140
7741	Db		TCTTCAATGTGTAGTTCGCGCAGCATGCTGGCAAAAGGCTGTACTATCTCACCGGT	7800
7141	Qy		GACCCACACACCCCTTTCGCGGGGTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
7801	Db		GACCCACACACCCCTTTCGCGGGGTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7860
7201	Qy		TCTTGCTTAGGCAACATCATATGATATGCGCCACCTTGTGGCAAGGATGATCCTGATG	7260
7861	Db		TCTTGCTTAGGCAACATCATATGATATGCGCCACCTTGTGGCAAGGATGATCCTGATG	7920
7261	Qy		ACTCATTTCTTCTCCATCTCTTAGCTCAGGAACAACTTGAAAAAGCCCTAGATGTCTAG	7320
7921	Db		ACTCATTTCTTCTCCATCTCTTAGCTCAGGAACAACTTGAAAAAGCCCTAGATGTCTAG	7980
7321	Qy		ATCTACGGGCGTGTACTCCATAGAGCACTTGACCTCAGATCATTCACGACTC	7380
7981	Db		ATCTACGGGCGTGTACTCCATAGAGCACTTGACCTCAGATCATTCACGACTC	8040
7381	Qy		CATGGGCTTAGCGCATTTTACATTCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
8041	Db		CATGGGCTTAGCGCATTTTACATTCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	8100
7441	Qy		TCAATGCTCAGGAAACTTGGGTTACCGGCTTTCGAGTCTGGAGACATCGGGCCAGAGT	7500
8101	Db		TCAATGCTCAGGAAACTTGGGTTACCGGCTTTCGAGTCTGGAGACATCGGGCCAGAGT	8160
7501	Qy		GTCCGGCTTAGGCTACTGTCCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTTC	7560
8161	Db		GTCCGGCTTAGGCTACTGTCCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTTC	8220
7561	Qy		AACCTGGCAGTAAAGGACCAAGCTCAAACTCACTCCATCCGGCTGCGTCCAGTTGGAT	7620
8221	Db		AACCTGGCAGTAAAGGACCAAGCTCAAACTCACTCCATCCGGCTGCGTCCAGTTGGAT	8280
7621	Qy		TTATCCAGCTGGTTCGTTGCTGGTTACAGCGGGGAGACATATATCACAGCTGTCTCGT	7680
8281	Db		TTATCCAGCTGGTTCGTTGCTGGTTACAGCGGGGAGACATATATCACAGCTGTCTCGT	8340
7681	Qy		GCCCGACCCCGCTGGTTCAATGGTGCCATCTCTACTTTCTGTAGGGGTAGGCATCTAT	7740
8341	Db		GCCCGACCCCGCTGGTTCAATGGTGCCATCTCTACTTTCTGTAGGGGTAGGCATCTAT	8400
7741	Qy		CTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTGTTT	7800
8401	Db		CTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTGTTT	8460
7801	Qy		TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
8461	Db		TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8520
7861	Qy		TTTTTCTCTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
8521	Db		TTTTTCTCTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8580
7921	Qy		TAGCTGTGAAGAGTCGTCAGCGGCTTGACTGCAGAGAGTGTCTGATCTAGGCTCTCTGC	7980
8581	Db		TAGCTGTGAAGAGTCGTCAGCGGCTTGACTGCAGAGAGTGTCTGATCTAGGCTCTCTGC	8640
7981	Qy		AGATCAAGT	7989

602	QY	CGACGGGGTTCTCTTTCGCGAGCTGTGCTGCAGCGTTGTCTCACTGAAGCGGGAAGGACTGGC	661
661	QY	TGCTATTGGCGAAAGTGTCCGGGCGAGGATCTCTCTCATCTCACTCACTTGTCTCTCTGCCGAGA	720
662	Db	TGCTATTGGGCGAAGTGTCCGGGCGAGGATCTCTCTCATCTCACTTGTCTCTCTGCCGAGA	721
721	QY	AAGTATCCATCATGGCTGATGCAATTCGGCGGCTGCTATACGCTTGATCGGCTACCTGCC	780
722	Db	AAGTATCCATCATGGCTGATGCAATTCGGCGGCTGCTATACGCTTGATCGGCTACCTGCC	781
781	QY	CATTTCGACCCCAAGCGGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCCGGTC	840
782	Db	CATTTCGACCCCAAGCGGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCCGGTC	841
841	QY	TTGTTCGATCAGGATGATCTGAGCAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTCG	900
842	Db	TTGTTCGATCAGGATGATCTGGAAGAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTCG	901
901	QY	CCAGGCTCAAGGCGCGCATCCGACGCGGAGGATCTCTGCTGTCACCCATCGCGCATGCCCT	960
902	Db	CCAGGCTCAAGGCGCGCATCCGACGCGGAGGATCTCTGCTGTCACCCATCGCGCATGCCCT	961
961	QY	GCTTTGCCGAATATCATGCTGGGAAATGGCGGCTTTCTGGAATCATCGACTGTGGCGCGC	1020
962	Db	GCTTTGCCGAATATCATGCTGGGAAATGGCGGCTTTCTGGAATCATCGACTGTGGCGCGC	1021
1021	QY	TGGGTGTGGCGGACCGCTATCAGGAATAGCTGTGGCTACCGGTGATTCGCGATTCGCGAGC	1080
1022	Db	TGGGTGTGGCGGACCGCTATCAGGAATAGCTGTGGCTACCGGTGATTCGCGATTCGCGAGC	1081
1081	QY	TTGGCGGCGAATGGGCTGACCGCTTCTGCTGTGTTTACGGTATCGCGCTCCCGATTCGC	1140
1082	Db	TTGGCGGCGAATGGGCTGACCGCTTCTGCTGTGTTTACGGTATCGCGCTCCCGATTCGC	1141
1141	QY	AGCGCATCGCTTCTATCGCTTCTTGAAGAGTCTCTTGAGTT-----TAAA	1188
1142	Db	AGCGCATCGCTTCTATCGCTTCTTGAAGAGTCTCTTGAGTT-----TAAA	1201
1189	QY	CAGACCAACCGTTTCCCTCTAGCGGGATCAATCCGCGGCTTCTGCTATATGTTATTT	1248
1202	Db	CAGACCAACCGTTTCCCTCTAGCGGGATCAATCCGCGGCTTCTGCTATATGTTATTT	1250
1249	QY	RACGTTACTGGCGGAAGCGGTTGGAAATAAGCGCGGTGTGCTATATGTTATTT	1308
1251	Db	RACGTTACTGGCGGAAGCGGTTGGAAATAAGCGCGGTGTGCTATATGTTATTT	1310
1309	QY	TCCACCATATTGCCGCTTTTGGCAATGTAGGGCCCGGAAACCTTGCGGCTGTCTCTTTG	1368
1311	Db	TCCACCATATTGCCGCTTTTGGCAATGTAGGGCCCGGAAACCTTGCGGCTGTCTCTTTG	1370
1369	QY	ACGAGCATCTAGGGGCTTTTCCCTCTCGCAAGGAATGCAAGTCTGTGTAATGTC	1428
1371	Db	ACGAGCATCTAGGGGCTTTTCCCTCTCGCAAGGAATGCAAGTCTGTGTAATGTC	1430
1429	QY	GTGAAGGAAGCAGTTCCCTCTGGAAGCTTTTGAAGCAAAAACAAGTCTGTAGCACCCCTT	1488
1431	Db	GTGAAGGAAGCAGTTCCCTCTGGAAGCTTTTGAAGCAAAAACAAGTCTGTAGCACCCCTT	1490
1489	QY	TGCAGGCAGCGGAACCCCGACCTTGGGACAGGTGCTCTCGGCGCAAAAGCCACGTGTA	1548
1491	Db	TGCAGGCAGCGGAACCCCGACCTTGGGACAGGTGCTCTCGGCGCAAAAGCCACGTGTA	1550
1549	QY	TAGATACACTGCAAGGGCGGCAACCCCGAGTGCACCGTGTGAGTTGGATAGTTGTG	1608
1551	Db	TAGATACACTGCAAGGGCGGCAACCCCGAGTGCACCGTGTGAGTTGGATAGTTGTG	1610
1609	QY	GAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCGAGAAG	1668
1611	Db	GAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCGAGAAG	1670
1669	QY	GTACCCCAATTGTATGGGATCTGATCTGGGCGCTCGGTGCACTGCTTTACATGTTTGTAG	1728
1671	Db	GTACCCCAATTGTATGGGATCTGATCTGGGCGCTCGGTGCACTGCTTTACATGTTTGTAG	1730

QY	1729	TCGAGGTTAA	AAAAAGCTCTAGGCCCCCGAAACACACGGGACGTGGTTTCCTTTGAAAAA	1789
Db	1731	TCGAGGTTAA	AAAAAGCTCTAGGCCCCCGAAACACACGGGACGTGGTTTCCTTTGAAAAA	1790
QY	1789	CACGATAATACCATG	-----	1803
Db	1791	CACGATAATACCATG	ACCGGAGATGCAGCATCGTCGGAGGCGCGGTTTCGTAGGT	1850
QY	1804	-----	-----	1803
Db	1851	CTGATACTCTTGACCTTGTCTACCGCACTATAAGCTGTTCTCGTAGGCTCATATGGTGG	1910	
QY	1804	-----	-----	1803
Db	1911	TTACAATATTTTATCACAGGCGCCGAGGCACATTGCAAGTGTGGATCCCCGCCCTCAAC	1970	
QY	1804	-----	-----	1803
Db	1971	GTTCCGGGGGCGCGATGCGTCACTCTCTCAGTSCGCGATCCACCCAGAGCTAATC	2030	
QY	1804	-----	-----	1803
Db	2031	TTTACCATCACCAAAATCTTGCTCGCCATACTCGTCCACTCATGGTGTCTCCAGGCTGGT	2090	
QY	1804	-----	-----	1803
Db	2091	ATAACCAAGTGCCGTACTTCTGTGCGCGCACACGGGCTCATTCGTGTGATGTCATGTGTGGT	2150	
QY	1804	-----	-----	1803
Db	2151	CGGAAGTTGCTGGGGGTCAATTATGTCCAAATGGCTCTCATGAAGTTGGCGGCTACGA	2210	
QY	1804	-----	-----	1803
Db	2211	GGTACGTACGTTTATGACCATCTCACCCCACTCGGGACTTGGGCCACGGGGCTACGA	2270	
QY	1804	-----	-----	1803
Db	2271	GACCTTTCGGTGGCAGTTGAGCCCGTCGTCTTCTCTCATATGGAGACCAAGGTTATCACC	2330	
QY	1804	-----	-----	1803
Db	2331	TGGGGGCGACACCGCGCGTGTGGGGACATCATCTTGGGCCTGCCCGTCTCGGCCGC	2390	
QY	1804	-----	-----	1803
Db	2391	AGGGGAGGGAGATACATCTGGGACGGCGACAGACGCTTTGAAGGGCAGGGTGGCGACTC	2450	
QY	1804	---GGCCCTATTACGGCCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCACT	1860	
Db	2451	CTCGCGCTATTATACGGCCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCACT	2510	
QY	1861	AGCCTCACAGCCGGGACAGNAACAGTTCGAGGGGAGGTCCAAGTGTCTCCACCGCA	1920	
Db	2511	AGCTTCACAGCCGGGACAGAAACAGTTCGAGGGGAGGTCCAAGTGTCTCCACCGCA	2570	
QY	1921	ACAAATCTTTCCTGGCGACCTGGTCAATCGCGTGTGTGGACTGTCTATCATGTGTC	1980	
Db	2571	ACAAATCTTTCCTGGCGACCTGGTCAATCGCGTGTGTGGACTGTCTATCATGTGTC	2630	
QY	1981	GGCTCAAGACCTTTCGGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC	2040	
Db	2631	GGCTCAAGACCTTTCGGGCCCAAGGGCCCAATCACCCAAATGTACACCAATGTGGAC	2690	
QY	2041	CAGACCTCTCGCTGGCAAGCCGCCCGGGCGGTTCCTTGAACCATGCACTTGC	2100	
Db	2691	CAGACCTCTCGCTGGCAAGCCGCCCGGGCGGTTCCTTGAACCATGCACTTGC	2750	
QY	2101	GGCAGCTCGACCTTACTTGGTTCACGAGCATGCCGATGTCAATTCGGTGGCGCGGG	2160	
Db	2751	GGCAGCTCGACCTTACTTGGTTCACGAGCATGCCGATGTCAATTCGGTGGCGCGGG	2810	

4971	TTTAAAGGTCAATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT	5039
4381	ATCCTCTCCCTCGCGCCCTAGTCGTGCGGGTCGTGTCGCGAGCGATACATGCGTCGCGAC	4440
5031	ATCCTCTCCCTCGCGCCCTAGTCGTGCGGGTCGTGTCGCGAGCGATACATGCGTCGCGAC	5090
4441	GTGGGCCGAGGAGGGGGCTGTCAGTGTGATGAAACCGGCTGATAGCGTTTCGCTTCGCGG	4500
5091	GTGGGCCGAGGAGGGGGCTGTCAGTGTGATGAAACCGGCTGATAGCGTTTCGCTTCGCGG	5150
4501	GGTAAACCACTCTCCCGCAGCACTATGTGCTGTGAGAGCACTGCTGAGCACTGTCACCT	4560
5151	GGTAAACCACTCTCCCGCAGCACTATGTGCTGTGAGAGCACTGCTGAGCACTGTCACCT	5210
4561	CAGATCCTCTTAGTCTTACCAATCACTCAGCTGCTGAAGAGGCTTACCAGTGTGATCAAC	4620
5211	CAGATCCTCTTAGTCTTACCAATCACTCAGCTGCTGAAGAGGCTTACCAGTGTGATCAAC	5270
4621	GAGGACTGCTCCAGCGCATGTCTCCGCTCGTGCTAAGAGATGTTTGGGATTTCGATATGC	4680
5271	GAGGACTGCTCCAGCGCATGTCTCCGCTCGTGCTAAGAGATGTTTGGGATTTCGATATGC	5330
4681	ACGGTGTGTACTGATTTCAAGACCTGGCTCCAGTCAAGCTCTGCGCGGATTCGCGGGA	4740
5331	ACGGTGTGTACTGATTTCAAGACCTGGCTCCAGTCAAGCTCTGCGCGGATTCGCGGGA	5390
4741	GTCCCTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGCGGGGCGACGGCATCATG	4800
5391	GTCCCTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGCGGGGCGACGGCATCATG	5450
4801	CAAAACCACTGCCATGTGAGAGCAGATCACCGGACATGTGAAACCGTTCATGAGG	4860
5451	CAAAACCACTGCCATGTGAGAGCAGATCACCGGACATGTGAAACCGTTCATGAGG	5510
4861	ATCGTGGGGCTAGACCTGATGATTAACAGCTGGCATGGAACATTCCTCCCATTAACCGTAC	4920
5511	ATCGTGGGGCTAGACCTGATGATTAACAGCTGGCATGGAACATTCCTCCCATTAACCGTAC	5570
4921	ACACGGGCGCCTGCACGCGCTCCCGCGCGCAAAATTTCTAGGGGCTGTGGGGGTG	4980
5571	ACACGGGCGCCTGCACGCGCTCCCGCGCGCAAAATTTCTAGGGGCTGTGGGGGTG	5630
4981	GCTGCTGAGGAGTACGTGGAGGTTACGCGGTGGGGATTTCCATAGTCAGCGGGCATG	5040
5631	GCTGCTGAGGAGTACGTGGAGGTTACGCGGTGGGGATTTCCATAGTCAGCGGGCATG	5690
5041	ACCCTGACAACTAAAGTCCCGTGTACGTTCCGGCCCCCGAATTTCTCACAGAGTG	5100
5691	ACCCTGACAACTAAAGTCCCGTGTACGTTCCGGCCCCCGAATTTCTCACAGAGTG	5750
5101	GATGGGTGCGGTTGCACAGGTACGCTCCAGCGTGCAAACCCCTCTACGGGAGGAGTGC	5160
5751	GATGGGTGCGGTTGCACAGGTACGCTCCAGCGTGCAAACCCCTCTACGGGAGGAGTGC	5810
5161	ACATTTCTCGTCCGGCTCAATCAATACCTGTTGGGTTCAGCTCCCATCGAGCCCGAA	5220
5811	ACATTTCTCGTCCGGCTCAATCAATACCTGTTGGGTTCAGCTCCCATCGAGCCCGAA	5870
5221	CGGACGTAGCAGTGTCTATTCCATGCTCACCGACCCCTCCACATACCGCGGAGACG	5280
5871	CGGACGTAGCAGTGTCTATTCCATGCTCACCGACCCCTCCACATACCGCGGAGACG	5930
5281	GCTAAGCGTAGCTGGCGAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCCAG	5340
5931	GCTAAGCGTAGCTGGCGAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCCAG	5990
5341	CTGCTCGCGCTTCTTGAAGGCAATGCACTACCGTATGACTCCCGGACCGTGCAC	5400
5991	CTGCTCGCGCTTCTTGAAGGCAATGCACTACCGTATGACTCCCGGACCGTGCAC	6050
5401	CTCATCGAGGCCAACTCTCTGTGGCGGAGGATGGGCGGAAATCATCACCGCGTGGAG	5460
6051	CTCATCGAGGCCAACTCTCTGTGGCGGAGGATGGGCGGAAATCATCACCGCGTGGAG	6110

QY	5461	TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGAGGAGATGAG	5520
Db	6111	TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGAGGAGATGAG	6170
QY	5521	AGGGAAGTATCCGTTTCGGCGGAGATCTCTCGGAGGTCCAGGAAATTCCTCCAGCGATG	5580
Db	6171	AGGGAAGTATCCGTTTCGGCGGAGATCTCTCGGAGGTCCAGGAAATTCCTCCAGCGATG	6230
QY	5581	CCCATATGGGCACGCCCGGATATCAACCTCCACTTGTAGTCTCGAAAGACCCGGAC	5640
Db	6231	CCCATATGGGCACGCCCGGATATCAACCTCCACTTGTAGTCTCGAAAGACCCGGAC	6290
QY	5641	TACGTCCCTCCAGTGGTACACGGGTGTCCATTGCCGCTGCCAAGGCCCTCCCGATACCA	5700
Db	6291	TACGTCCCTCCAGTGGTACACGGGTGTCCATTGCCGCTGCCAAGGCCCTCCCGATACCA	6350
QY	5701	CCTCCACGGAGAAAGAGACGGTTGTCTGTGCAGAAATCTACCGTGTCTTCTGCGCTTGGCG	5760
Db	6351	CCTCCACGGAGAAAGAGACGGTTGTCTGTGCAGAAATCTACCGTGTCTTCTGCGCTTGGCG	6410
QY	5761	GAGTCTCCGCCAACAAAGACCTTCGGCAGCTCCGAATCGTTCGAGAAATCTACCGTGTCTTCTGCGCTTGGCG	5820
Db	6411	GAGTCTCCGCCAACAAAGACCTTCGGCAGCTCCGAATCGTTCGAGAAATCTACCGTGTCTTCTGCGCTTGGCG	6470
QY	5821	ACGGCTCTCTCTGACCAAGCCCTCCGACGACGGCGACCGCGGATCCCGATCTCAGCAGCGGTCTTGG	5880
Db	6471	ACGGCTCTCTCTGACCAAGCCCTCCGACGACGGCGACCGCGGATCCCGATCTCAGCAGCGGTCTTGG	6530
QY	5881	TCCTCCATGCCGCCCTTTGAGGGGAGCGGGGATCCCGATCTCAGCAGCGGTCTTGG	5940
Db	6531	TCCTCCATGCCGCCCTTTGAGGGGAGCGGGGATCCCGATCTCAGCAGCGGTCTTGG	6590
QY	5941	CTACACGTAAAGCAGGAGGCTAGTGGAGCGTCTGTCTGTCTGATGTCGATGTCCTACACATGG	6000
Db	6591	CTACACGTAAAGCAGGAGGCTAGTGGAGCGTCTGTCTGTCTGATGTCGATGTCCTACACATGG	6650
QY	6001	ACAGCGCCCTGTATCAGCCATCGCTCGCGGAGGAAACCAAGCTGCCCATCATGCACTG	6060
Db	6651	ACAGCGCCCTGTATCAGCCATCGCTCGCGGAGGAAACCAAGCTGCCCATCATGCACTG	6710
QY	6061	AGCAACTCTTTCGTCCGTACACAACTTGGTCTATGTACAACTCTCGCAGCGCAAGC	6120
Db	6711	AGCAACTCTTTCGTCCGTACACAACTTGGTCTATGTACAACTCTCGCAGCGCAAGC	6770
QY	6121	CTCGCGCAGAAAGGTACCTTTGACAGACTGCAAGTCTCGGACGACACTACCGGAC	6180
Db	6771	CTCGCGCAGAAAGGTACCTTTGACAGACTGCAAGTCTCGGACGACACTACCGGAC	6830
QY	6181	GTGCTCAAGGAGATGAAGCGGAAGCGTCCAAGTTAAGGCTTAACTCTATCCGTTGGAG	6240
Db	6831	GTGCTCAAGGAGATGAAGCGGAAGCGTCCAAGTTAAGGCTTAACTCTATCCGTTGGAG	6890
QY	6241	GAAGCTCTGAAGCTGACGCCCCACATTCGGGCAGATCTAAATTTGGCTATGGGCCAAAG	6300
Db	6891	GAAGCTCTGAAGCTGACGCCCCACATTCGGGCAGATCTAAATTTGGCTATGGGCCAAAG	6950
QY	6301	GACGTCCGGAACCTATCCAGCAAGCGCGTTAAACCAATCCCGTCCGTGTGGAGACTTG	6360
Db	6951	GACGTCCGGAACCTATCCAGCAAGCGCGTTAAACCAATCCCGTCCGTGTGGAGACTTG	7010
QY	6361	CTGGAAGACACTGAGACCAAAATTTGACACCACTCATGCGAAAAATGAGGTTTCTGCG	6420
Db	7011	CTGGAAGACACTGAGACCAAAATTTGACACCACTCATGCGAAAAATGAGGTTTCTGCG	7070
QY	6421	GTCCAAACGAGAGGGGGCGGCAAGCTCGCCTTATCGTATTTCCAGATTTGGGG	6480
Db	7071	GTCCAAACGAGAGGGGGCGGCAAGCTCGCCTTATCGTATTTCCAGATTTGGGG	7130
QY	6481	GTTTCGTGTGCGCAAAAAATGGCCCTTTACGATGTGGTCTCCACCTCCCTCAGGCCGTG	6540
Db	7131	GTTTCGTGTGCGCAAAAAATGGCCCTTTACGATGTGGTCTCCACCTCCCTCAGGCCGTG	7190

QY	6541	ATGGGCTCTTCATACCGGATCCAAATCTCTCTCTGAGACGCGGTCGAGTTCCTCTGTAAT	6600
Db	7191	ATGGGCTCTTCATACCGGATCCAAATCTCTCTCTGAGACGCGGTCGAGTTCCTGTAAT	7250
QY	6601	GCCTGAAAGCGAAGAAATGCCTATGGCTTCGCATATGACACCGCTGTTTGTGACTCA	6660
Db	7251	GCCTGAAAGCGAAGAAATGCCTATGGCTTCGCATATGACACCGCTGTTTGTGACTCA	7310
QY	6661	ACGCTCACTGAGAAATGACATCCGCTGTTGAGGAGTCAATCTACAAATGTTGTGACTGGCC	6720
Db	7311	ACGCTCACTGAGAAATGACATCCGCTGTTGAGGAGTCAATCTACAAATGTTGTGACTGGCC	7370
QY	6721	CCCGAAGCCAGACAGGCCATAGAGTGCCTCAGAGCGGCTTACATCGGGGGCCCCCTG	6780
Db	7371	CCCGAAGCCAGACAGGCCATAGAGTGCCTCAGAGCGGCTTACATCGGGGGCCCCCTG	7430
QY	6781	ACTAATCTAAAGGCGAGAACTCGGCTATCGCGGTCGCGCGAGCGGTGTACTGACG	6840
Db	7431	ACTAATCTAAAGGCGAGAACTCGGCTATCGCGGTCGCGCGAGCGGTGTACTGACG	7490
QY	6841	ACCAGCTGCGGTAAATACCCCTCACATGTTACTTGAAGCCGCTCGCGGCTGTGAGCTGG	6900
Db	7491	ACCAGCTGCGGTAAATACCCCTCACATGTTACTTGAAGCCGCTCGCGGCTGTGAGCTGG	7550
QY	6901	AAGCTCCAGGACTGCAGATGCTGCTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	6960
Db	7551	AAGCTCCAGGACTGCAGATGCTGCTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC	7610
QY	6961	GCGGGACCCAGAGGAGGCGAGCTACGGGCTTTCACGGAGGCTATGACTAGATAC	7020
Db	7611	GCGGGACCCAGAGGAGGCGAGCTACGGGCTTTCACGGAGGCTATGACTAGATAC	7670
QY	7021	TCTGCCCCCTCGGGACCCGCCAAACCAAGTAACGATTCGAGTTGGATTGATAACATATGC	7080
Db	7671	TCTGCCCCCTCGGGACCCGCCAAACCAAGTAACGATTCGAGTTGGATTGATAACATATGC	7730
QY	7081	TCCTCCAAATGTCAGTGGCGCAGATGCATCTGCGCAAGGGTGTACTATCTCAACCGT	7140
Db	7731	TCCTCCAAATGTCAGTGGCGCAGATGCATCTGCGCAAGGGTGTACTATCTCAACCGT	7790
QY	7141	GACCCACACCCCTTGGCGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
Db	7791	GACCCACACCCCTTGGCGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7850
QY	7201	TCCTGGCTAGGCAACATCATCATATGATGCGCCACCTTGTGGGCAAGATGATCTGATG	7260
Db	7851	TCCTGGCTAGGCAACATCATCATATGATGCGCCACCTTGTGGGCAAGATGATCTGATG	7910
QY	7261	ACTCAATTTCTTCATCTCTAGTTCAGGACCACTTGAAGGCTTGAAGGCTTGAAGGCTT	7320
Db	7911	ACTCAATTTCTTCATCTCTAGTTCAGGACCACTTGAAGGCTTGAAGGCTTGAAGGCTT	7970
QY	7321	ATCTAGGGGCTGTTACTTCCATTTAGGACCACTTGAAGGCTTGAAGGCTTGAAGGCTT	7380
Db	7971	ATCTAGGGGCTGTTACTTCCATTTAGGACCACTTGAAGGCTTGAAGGCTTGAAGGCTT	8030
QY	7381	CATGGCTTAGGCGATTTTCACTCCATAGTTACTTCCAGGTGAGATCAATAGGTTGGT	7440
Db	8031	CACGGCTTAGGCGATTTTCACTCCATAGTTACTTCCAGGTGAGATCAATAGGTTGGT	8090
QY	7441	TCATGCTCAGGAACTTGGGTTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAT	7500
Db	8091	TCATGCTCAGGAACTTGGGTTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAT	8150
QY	7501	GTCCGCTAGGCTTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACTCTTC	7560
Db	8151	GTCCGCTAGGCTTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACTCTTC	8210
QY	7561	AACTGGGCGTAAAGGACAAAGCTCAACTCACTCCAGTCCCGCTGGTCCAGTTGGAT	7620
Db	8211	AACTGGGCGTAAAGGACAAAGCTCAACTCACTCCAGTCCCGCTGGTCCAGTTGGAT	8270
QY	7621	TTATCCAGCTGGTTCGTTGCTGTTTACAGCGGGGAGACATATATACAGCCTGCTCTCGT	7680
Db	8271	TTATCCAGCTGGTTCGTTGCTGTTTACAGCGGGGAGACATATATACAGCCTGCTCTCGT	8330
QY	7681	GCCCGACCCCGCTGGTTCATGTCGTGCTTACCTTCTGTTAGGGGTAGGCACTAT	7740
Db	8331	GCCCGACCCCGCTGGTTCATGTCGTGCTTACCTTCTGTTAGGGGTAGGCACTAT	8390
QY	7741	CTACTCCCAACCGATGAACCGGGAGCTAAACACCTCCAGGCCAATAGGCCATCTCTGTTT	7800
Db	8391	CTACTCCCAACCGATGAACCGGGAGCTAAACACCTCCAGGCCAATAGGCCATCTCTGTTT	8450
QY	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	8451	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8510
QY	7861	TTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT	7920
Db	8511	TTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT	8570
QY	7921	TAGCTGTAAAGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	7980
Db	8571	TAGCTGTAAAGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	8630
QY	7981	AGATCAAGT 7989	
Db	8631	AGATCAAGT 8639	

RESULT 9

US-10-029-907-24
 ; Sequence 24, Application US/10029907
 ; Patent No. 6706874
 ; GENERAL INFORMATION:
 ; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
 ; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
 ; TITLE OF INVENTION: HEPATITIS C VIRUS
 ; FILE REFERENCE: 13/083
 ; CURRENT APPLICATION NUMBER: US/10/029,907
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 60/257,857
 ; PRIOR FILING DATE: 2000-12-22
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 8638
 ; TYPE: DNA
 ; ORGANISM: HCV
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1802)...(8407)
 ; US-10-029-907-24

Query Match 91.0%; Score 7272.8; DB 4; Length 8638;
 Best Local Similarity 92.2%; Pred. No. 0;
 Matches 7975; Conservative 0; Mismatches 2; Indels 671; Gaps 3;

QY	2	CCAGCCCCCGATGGGGGCGACATCCACATAGATCACTCCCTCTGTAGGAACTACTGT	61
Db	2	CCAGCCCCCGATGGGGGCGACATCCACATAGATCACTCCCTCTGTAGGAACTACTGT	61
QY	62	CTTTCACGAGAAAGCGCTTAGCCATGGCTTAGTATGAGTGTCTGAGCCTCCAGACC	121
Db	62	CTTTCACGAGAAAGCGCTTAGCCATGGCTTAGTATGAGTGTCTGAGCCTCCAGACC	121
QY	122	CCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGGCAGG	181
Db	122	CCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATGGCAGG	181
QY	182	ACGACCGGGTCTTTCTTTGGATCAACCGCTCAATGCTCGAGATTTGGCGGTGCCCGG	241
Db	182	ACGACCGGGTCTTTCTTTGGATCAACCGCTCAATGCTCGAGATTTGGCGGTGCCCGG	241
QY	242	CGAGACTGCTAGCGCGAGTGTGTTGGGTGCGGAAGGCCCTTGTGTTACTGCTGATAGGG	301

Db 242 CGAGCTGCTAGCCGAGTAGTGTGGTTCGGAAGGCCCTTGTGGTACTGCTGATAGG 301
QY 302 TGCTTGGAGTGGCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAAC 361
Db 302 TGCTTGGAGTGGCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAAC 361
QY 362 TCAAGAAAAACAAMAGGCGCCCATGATTAAGCAAGATGGATTGACCCAGGTTCTCC 421
Db 362 TCAAGAAAAACAAMAGGCGCCCATGATTAAGCAAGATGGATTGACCCAGGTTCTCC 421
QY 422 GGCCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCACACAGACATCCGCTGCTC 481
Db 422 GGCCGCTTGGTGGAGAGGCTATTCCGCTATGACTGGGCACACAGACATCCGCTGCTC 481
QY 482 TGATGCGCGCTGTTCCGCTGTACGCGAGGCGCCCGGTTCTTTTGTCAAGACCGA 541
Db 482 TGATGCGCGCTGTTCCGCTGTACGCGAGGCGCCCGGTTCTTTTGTCAAGACCGA 541
QY 542 CCTGTCCGCTGCCCTCAATGAATGCTCAGCAGCAGGCGAGCGGGCTATCGTGGCTGCCAC 601
Db 542 CCTGTCCGCTGCCCTCAATGAATGCTCAGCAGCAGGCGAGCGGGCTATCGTGGCTGCCAC 601
QY 602 GACGGCGTTCTTCCGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGAGGACTGGCT 661
Db 602 GACGGCGTTCTTCCGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGAGGAGGACTGGCT 661
QY 662 GCTATTGGCGAAGTGCCTGGCGAGGATCTCTGTCTCATCTCACTTGTCTTCCGCGAGAA 721
Db 662 GCTATTGGCGAAGTGCCTGGCGAGGATCTCTGTCTCATCTCACTTGTCTTCCGCGAGAA 721
QY 722 AGTATCCATCATGCTGTGATGCAATGCGCGGCTGATAGCTTGTATCGGGTACCTGCC 781
Db 722 AGTATCCATCATGCTGTGATGCAATGCGCGGCTGATAGCTTGTATCGGGTACCTGCC 781
QY 782 ATTGCACCAAGCAAGCAACATCGCATCGAGCAGCAGTACTCGGATGGAAGCGGCTCT 841
Db 782 ATTGCACCAAGCAAGCAACATCGCATCGAGCAGCAGTACTCGGATGGAAGCGGCTCT 841
QY 842 TGTGATCAGATGATCTGGAAGAGCATCAGGGGCTCGCGCCAGCGCAACTGTTCCG 901
Db 842 TGTGATCAGATGATCTGGAAGAGCATCAGGGGCTCGCGCCAGCGCAACTGTTCCG 901
QY 902 CAGGCTCAAGCGCGCATGCCCGAGCGGAGGATCTCGTGTGACCCATGCGGATGCTG 961
Db 902 CAGGCTCAAGCGCGCATGCCCGAGCGGAGGATCTCGTGTGACCCATGCGGATGCTG 961
QY 962 CTTGCCGAATATCATGTTGGAATGCGCGTTTCTTGGATTTCATCGACTGCGCGGCT 1021
Db 962 CTTGCCGAATATCATGTTGGAATGCGCGTTTCTTGGATTTCATCGACTGCGCGGCT 1021
QY 1022 GGGTGTGGCGACCGCTATCAGGACATAGGCTTGGCTACCGCTGATATTGCTGAAGAGCT 1081
Db 1022 GGGTGTGGCGACCGCTATCAGGACATAGGCTTGGCTTGGCTACCGCTGATATTGCTGAAGAGCT 1081
QY 1082 TGGCGGCAATGGGCTGACCGCTTCTCGTGTCTTACGCTATCGCGCTCCCGATCGCA 1141
Db 1082 TGGCGGCAATGGGCTGACCGCTTCTCGTGTCTTACGCTATCGCGCTCCCGATCGCA 1141
QY 1142 GGCATCGCTTCTATCGCTTCTTGAACAGTGTCTTCTGAGTT-----TAAAC 1189
Db 1142 GGCATCGCTTCTATCGCTTCTTGAACAGTGTCTTCTGAGTT-----TAAAC 1189
QY 1190 AGACCAACAGGTTTCCCTTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCTA 1249
Db 1202 AGACCAACAGGTTTCCCTTAGCGGATCAATTCG-----CCCCCCCCCTA 1250
QY 1250 ACCTTACTGCGGAGCGCTTGGATAGGCGGCTGCGGTTGCTATATGTTATTTT 1309
Db 1251 ACCTTACTGCGGAGCGCTTGGATAGGCGGCTGCGGTTGCTATATGTTATTTT 1310
QY 1310 CCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTTCTTGA 1369
|||

Db 1311 CCACCATATTGCGCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTTCTTCTGA 1370
QY 1370 CGAGCATTCCTAGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTTGAATGTCG 1429
Db 1371 CGAGCATTCCTAGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTTGAATGTCG 1430
QY 1430 TGAAGGAAGCAGTTCCTCTGGAAGCTTTCTGAAGCAAAACAACCTGTGTAGCAGCCCTTT 1489
Db 1431 TGAAGGAAGCAGTTCCTCTGGAAGCTTTCTGAAGCAAAACAACCTGTGTAGCAGCCCTTT 1490
QY 1490 GCAGGAGGGAACCCCCACCTTGGCGACAGGTGCTCTGCGGCCAAAGGCCAGCTGTAT 1549
Db 1491 GCAGGAGGGAACCCCCACCTTGGCGACAGGTGCTCTGCGGCCAAAGGCCAGCTGTAT 1550
QY 1550 AAGATACACTGCTCAAGGCGGCAAAACCCAGTGCACCTGTGTAGTGGATAGTTGTGG 1609
Db 1551 AAGATACACTGCTCAAGGCGGCAAAACCCAGTGCACCTGTGTAGTGGATAGTTGTGG 1610
QY 1610 AAGAGTCAAAATGGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGGATGCCAGAAG 1669
Db 1611 AAGAGTCAAAATGGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGGATGCCAGAAG 1670
QY 1670 TACCCATTTGATGGATCTGATCTGGGCGCTCGGTCACATGCTTTACATGTTTATG 1729
Db 1671 TACCCATTTGATGGATCTGATCTGGGCGCTCGGTCACATGCTTTACATGTTTATG 1730
QY 1730 CGAGTTTAAAAACCTCTAGGCCCCCGAAACCAAGGGGACGTGTTTCTTTGAAAAAC 1789
Db 1731 CGAGTTTAAAAACCTCTAGGCCCCCGAAACCAAGGGGACGTGTTTCTTTGAAAAAC 1790
QY 1790 ACGATAATACCATG----- 1803
Db 1791 ACGATAATACCATGACCGGAGATGCGAGCATCGTGGGAGCGCGTTCGTTAGTTC 1850
QY 1804 ----- 1803
Db 1851 TGATACCTTGACCTTGTACCGCACTATAAGCTGTTCTCGCTAGGCTCATATGTTG 1910
QY 1804 ----- 1803
Db 1911 TACAATATTTTATCACAGGCGGAGGACACTTGAAGTGGATCCCGCCCTCAACG 1970
QY 1804 ----- 1803
Db 1971 TCGGGGGGCGCGATGCGGTCATCTCTCAAGTGGGATCCACCGAGACTAATCT 2030
QY 1804 ----- 1803
Db 2031 TTACCATCACAAAATCTTGTCTGCCATATCTCGGTCCACTCATGTTGCTCCAGGCTG 2090
QY 1804 ----- 1803
Db 2091 TAAACAAAGTGGCTACTTCTGTGGCGACACCGGCTCATTCGTGATGATGCTGTTG 2150
QY 1804 ----- 1803
Db 2151 GGAAGTTGCTGGGGTCAATATGTCAAAATGCTCTCATGAAGTTGGCGGCACTGACAG 2210
QY 1804 ----- 1803
Db 2211 GTACGTACGTTTATGACCAATCTACCCACTGCGGACTGGGCCACCGGGCTACGAG 2270
QY 1804 ----- 1803
Db 2271 ACCTTGGGTGGCAGTTGAGCCGCTGCTTCTCTGATATGAGACCAAGGTTTATCACCT 2330
QY 1804 ----- 1803
Db 2331 GGGGGGACAGACCCCGCGGTGTGGGACATCATCTTGGGCTGCGCGCTCCGCCGCA 2390
QY 1804 ----- 1803
Db 2391 GGGGAGGAGATACATCTGGGACCGGACAGACCTTTGAAGGGGAGGGGTGGCGACTCC 2450

QY	1804	--GGCCCTATTACGCCCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCACTA	1861
Db	2451	TCGGGCCCTATTACGCCCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCACTA	2510
QY	1862	GCCTCACAGGCGGACAGGAAACAGGTCGAGGGGAGGTCCAGTGTCTCCACCGCAA	1921
Db	2511	GCCTCACAGGCGGACAGGAAACAGGTCGAGGGGAGGTCCAGTGTCTCCACCGCAA	2570
QY	1922	CACAACTCTTCTGGGACCTCGCTCAATGGCGTGTGGACTGTCTATCATGTGTGCG	1981
Db	2571	CACAACTCTTCTGGGACCTCGCTCAATGGCGTGTGGACTGTCTATCATGTGTGCG	2630
QY	1982	GCTCAAGACCTTTCGCGGCCCAAGGCCCCAATCAACCAATGTACCAATGTGAGCC	2041
Db	2631	GCTCAAGACCTTTCGCGGCCCAAGGCCCCAATCAACCAATGTACCAATGTGAGCC	2690
QY	2042	AGGACCTCGTGGCTGGCAAGGCCGCCCGGGCGGCTTCTTGACACCATGCACTGCG	2101
Db	2691	AGGACCTCGTGGCTGGCAAGGCCGCCCGGGCGGCTTCTTGACACCATGCACTGCG	2750
QY	2102	GCAGCTCGACCTTTACTTGTTCACGAGGATGCCGATGTCAATCCGGTGCAGCGCGG	2161
Db	2751	GCAGCTCGACCTTTACTTGTTCACGAGGATGCCGATGTCAATCCGGTGCAGCGCGG	2810
QY	2162	GCACACAGCGGGAGGCTACTCTCCCGGAGGCCGCTCTCTACTTTGAAGGCTCTTCGG	2221
Db	2811	GCACACAGCGGGAGGCTACTCTCCCGGAGGCCGCTCTCTACTTTGAAGGCTCTTCGG	2870
QY	2222	GCAGTCCACTGCTCGGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCGGTGCA	2281
Db	2871	GCAGTCCACTGCTCGGCCCTCGGGGACGCTGTGGGCACTTTTCGGGCTGCGGTGCA	2930
QY	2282	CCGAGGGGTGCGAAGCGGTGACTTTGTACCCGTCGAGTCTATGGAACCACTATGC	2341
Db	2931	CCGAGGGGTGCGAAGCGGTGACTTTGTACCCGTCGAGTCTATGGAACCACTATGC	2990
QY	2342	GGTCCCGGCTCTTCCAGGACAACTCTGTCCTCCCGCGGTACCGGACATCCAGGTGG	2401
Db	2991	GGTCCCGGCTCTTCCAGGACAACTCTGTCCTCCCGCGGTACCGGACATCCAGGTGG	3050
QY	2402	CCCATCTACCGCCCTACTGGTAGCGGCAAGAGCACTTAAGTGCGGCTGCGGTATGAG	2461
Db	3051	CCCATCTACCGCCCTACTGGTAGCGGCAAGAGCACTTAAGTGCGGCTGCGGTATGAG	3110
QY	2462	CCCAAGGTATAGGTGCTTGTCTGAACCCGTCGCGGCCCAACCTAGTGTTCGGGG	2521
Db	3111	CCCAAGGTATAGGTGCTTGTCTGAACCCGTCGCGGCCCAACCTAGTGTTCGGGG	3170
QY	2522	CGTATATGTCTAAGGCACATGATATCGACCCCTAAATCAGAACCGGGTAAGGACATCA	2581
Db	3171	CGTATATGTCTAAGGCACATGATATCGACCCCTAAATCAGAACCGGGTAAGGACATCA	3230
QY	2582	CCACGGGTGCCCCATCAGTACTCCACCTATGGCAAGTTTCTTGGCGGCTGCTGTGCT	2641
Db	3231	CCACGGGTGCCCCATCAGTACTCCACCTATGGCAAGTTTCTTGGCGGCTGCTGTGCT	3290
QY	2642	CTGGGGGCGCCTATGACATCAATAATGTGATGAGTSCCACTCACTGACTCGACCACTA	2701
Db	3291	CTGGGGGCGCCTATGACATCAATAATGTGATGAGTSCCACTCACTGACTCGACCACTA	3350
QY	2702	TCCTGGGCTCGGCACAGTCTTGCAACAGCGGAGAGGCTGAGCGGACTCGTCTGTC	2761
Db	3351	TCCTGGGCTCGGCACAGTCTTGCAACAGCGGAGAGGCTGAGCGGACTCGTCTGTC	3410
QY	2762	TGCGCACCGGTACGCCCTCGGGATCGGTACCGTGCACATCCAAATCGAGGAGGTGG	2821
Db	3411	TGCGCACCGGTACGCCCTCGGGATCGGTACCGTGCACATCCAAATCGAGGAGGTGG	3470
QY	2822	CTCTGTCCAGCACTGGAGAAATCCCTTTTATGSCAAAGGCATCCCATCGAGCACTCA	2881
Db	3471	CTCTGTCCAGCACTGGAGAAATCCCTTTTATGSCAAAGGCATCCCATCGAGCACTCA	3530
QY	2882	AGGGGGGAGGACCTCATTTTCTGCCATTCACAGAGAAATGTGATGAGTCCGCGCA	2941
Db	3531	AGGGGGGAGGACCTCATTTTCTGCCATTCACAGAGAAATGTGATGAGTCCGCGCA	3590
QY	2942	AGTGTCCGGCTCGGACTCAATGTGTAGCATATTCAGGGGCTTGTATGATCCGTCA	3001
Db	3591	AGTGTCCGGCTCGGACTCAATGTGTAGCATATTCAGGGGCTTGTATGATCCGTCA	3650
QY	3002	TACCAACTAGCGGAGACGTCATTTGTCTGAGCAACCGGACGCTTAATGACGGCTTTACG	3061
Db	3651	TACCAACTAGCGGAGACGTCATTTGTCTGAGCAACCGGACGCTTAATGACGGCTTTACG	3710
QY	3062	GGGATTTCCGACTCGATGATCGATGATGATGATGATGATGATGATGATGATGATGATG	3121
Db	3711	GGGATTTCCGACTCGATGATCGATGATGATGATGATGATGATGATGATGATGATGATG	3770
QY	3122	TGGAACCGGACCTTACCATTTGAGACGACCGTGTGCAACGCGGTGTACAGTGTG	3181
Db	3771	TGGAACCGGACCTTACCATTTGAGACGACCGTGTGCAACGCGGTGTACAGTGTG	3830
QY	3182	AGCGGCGAGGACGAGTGTGAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGAG	3241
Db	3831	AGCGGCGAGGACGAGTGTGAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGAG	3890
QY	3242	AACGGCCCTCGGGCATTTCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3301
Db	3891	AACGGCCCTCGGGCATTTCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3950
QY	3302	CTTTGTACGAGCTCAGCCCGCGAGACCTCAGTTAGTTTTCGGGCTTACTTAAACACAC	3361
Db	3951	CTTTGTACGAGCTCAGCCCGCGAGACCTCAGTTAGTTTTCGGGCTTACTTAAACACAC	4010
QY	3362	CAGGTTTCCCGCTGTCGACGACCATCTGGAGTCTGGGAGAGGCTTTTACAGGCTTCA	3421
Db	4011	CAGGTTTCCCGCTGTCGACGACCATCTGGAGTCTGGGAGAGGCTTTTACAGGCTTCA	4070
QY	3422	CCCAATAGAGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGAGCAACTTCCCTTACC	3481
Db	4071	CCCAATAGAGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGAGCAACTTCCCTTACC	4130
QY	3482	TGTTAGCATACAGGCTACGCTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGACC	3541
Db	4131	TGTTAGCATACAGGCTACGCTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGACC	4190
QY	3542	AAATGTGAAGTGTCTCATACGGCTTAAAGCTTACGCTGACGGGCAAGCCCTGCTGT	3601
Db	4191	AAATGTGAAGTGTCTCATACGGCTTAAAGCTTACGCTGACGGGCAAGCCCTGCTGT	4250
QY	3602	ATAGCTGGGAGCCGTTCAAAACGAGGTTTACCCACACACCCCATTAACCAATACATCA	3661
Db	4251	ATAGCTGGGAGCCGTTCAAAACGAGGTTTACCCACACACCCCATTAACCAATACATCA	4310
QY	3662	TGGCATGATGTCGGCTGACCTGAGGTCGTCACGAGCACCTGGGTGCTGGTAGGCGAG	3721
Db	4311	TGGCATGATGTCGGCTGACCTGAGGTCGTCACGAGCACCTGGGTGCTGGTAGGCGAG	4370
QY	3722	TCCTAGCAGCTTCGGCCGCTATGCTGACAAACGAGGAGGCTTATTTGGGCGAGGA	3781
Db	4371	TCCTAGCAGCTTCGGCCGCTATGCTGACAAACGAGGAGGCTTATTTGGGCGAGGA	4430
QY	3782	TCATCTTGTTCGGGAAGCGGCTCATTTCCGACAGGGAAGTCTTTTACCGGAGTTCG	3841
Db	4431	TCATCTTGTTCGGGAAGCGGCTCATTTCCGACAGGGAAGTCTTTTACCGGAGTTCG	4490
QY	3842	ATGAGATGGAAGTTCGGCTTCACTCTCCCTTATCGAAGAGGAAATGACGCTCGCG	3901
Db	4491	ATGAGATGGAAGTTCGGCTTCACTCTCCCTTATCGAAGAGGAAATGACGCTCGCG	4550
QY	3902	AACAAATTCAAAGAGAGGCTCGGTTGCTGCAACAGCCACCAAGCAGGAGGCTG	3961
Db	4551	AACAAATTCAAAGAGAGGCTCGGTTGCTGCAACAGCCACCAAGCAGGAGGCTG	4610
QY	3962	CTGCTCCGCTGGTGAATCCAGTGGCGGACCTTCGAAGGCTTCTGGGCGAAGCATATGT	4021

Db 4611 CTGCTCCGTTGGTGGATCCAAATGGCGGACCCCTCGAAGCCTTCTGGCGGAACATATGT 4670
QY 4022 GGAATTTCAATCAGCGGATACAAATATTTAGCAGCTTGTCCACTCTCGCTCGGCAACCCCG 4081
Db 4671 GGAATTTCAATCAGCGGATACAAATATTTAGCAGCTTGTCCACTCTCGCTCGGCAACCCCG 4730
QY 4082 CGATAGCATCAGTATGGGATTCACAGCTCTATACACGCGCTCACCACCCCAACATA 4141
Db 4731 CGATAGCATCAGTATGGGATTCACAGCTCTATACACGCGCTCACCACCCCAACATA 4790
QY 4142 CCCTCTCTGTTTAACTCCCTGGGGGATGGTGGCGCCCAACTTGTCTCTCCAGCGCTG 4201
Db 4791 CCCTCTCTGTTTAACTCCCTGGGGGATGGTGGCGCCCAACTTGTCTCTCCAGCGCTG 4850
QY 4202 CTTCTCTCTTCTAGCGCGCGCATCGCTGGAGCGCTGTGGAGCGCTGTTGGAGCATAGGCCCTTGGGA 4910
Db 4851 CTTCTCTCTTCTAGCGCGCGCATCGCTGGAGCGCTGTGGAGCGCTGTTGGAGCATAGGCCCTTGGGA 4970
QY 4262 AGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCTCGTGGCCT 4321
Db 4911 AGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCTCGTGGCCT 4970
QY 4322 TTAAGTTCATGAGCGCGGAGATGCCCTCCACGAGACCTGTTAACTTAACTTCCCTGCTA 4381
Db 4971 TTAAGTTCATGAGCGCGGAGATGCCCTCCACGAGACCTGTTAACTTAACTTCCCTGCTA 5030
QY 4382 TCCTCTCCCTGGCGCCTAGTCTGCGGGTGTGTGGCGAGCGGATCTGGCTGGGCAAG 4441
Db 5031 TCCTCTCCCTGGCGCCTAGTCTGCGGGTGTGTGGCGAGCGGATCTGGCTGGGCAAG 5090
QY 4442 TGGGCCACAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATACGCTTCGCTTCGCGGG 4501
Db 5091 TGGGCCACAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATACGCTTCGCTTCGCGGG 5150
QY 4502 GTAAACCACTCTCCCGACGCACTATGCTGAGAGCGGCTGAGAGCGGCTGACGCTGTCATC 4561
Db 5151 GTAAACCACTCTCCCGACGCACTATGCTGAGAGCGGCTGAGAGCGGCTGACGCTGTCATC 5210
QY 4562 AGATCTCTCTAGTCTTACCACTACTAGCTGCTGAGAGCGGCTTACCAGTGGATCAACG 4621
Db 5211 AGATCTCTCTAGTCTTACCACTACTAGCTGCTGAGAGCGGCTTACCAGTGGATCAACG 5270
QY 4622 AGGACTGCTCCAGCCATGCTCCGGCTCGTGGCTPAAGAGATGTTTGGGATGGATATGCA 4681
Db 5271 AGGACTGCTCCAGCCATGCTCCGGCTCGTGGCTPAAGAGATGTTTGGGATGGATATGCA 5330
QY 4682 CGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCCAAGCTCCTGCGCGGATTCGCGGAG 4741
Db 5331 CGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCCAAGCTCCTGCGCGGATTCGCGGAG 5390
QY 4742 TCCCTCTCTCTCATGTCACACGTTGGGTPAACGGAGTCTGCGCGGCGGACGGCATCATGC 4801
Db 5391 TCCCTCTCTCTCATGTCACACGTTGGGTPAACGGAGTCTGCGCGGCGGACGGCATCATGC 5450
QY 4802 ARAACCACTGCCCATGTGGAGCAGATCAACCGGACATGTGAAAAACGGTTCCATGAGGA 4861
Db 5451 ARAACCACTGCCCATGTGGAGCAGATCAACCGGACATGTGAAAAACGGTTCCATGAGGA 5510
QY 4862 TCGTGGGCGCTAGGACTGCTGATTAACACGTTGGGATGGACATTTCCCCCATTAACCGCGTGA 4921
Db 5511 TCGTGGGCGCTAGGACTGCTGATTAACACGTTGGGATGGACATTTCCCCCATTAACCGCGTGA 5570
QY 4922 CACGGGCGCTGCAACCGCTCCCGCGCGCAAAATTAATCTAGGCGCTGTGGCGGCTG 4981
Db 5571 CACGGGCGCTGCAACCGCTCCCGCGCGCAAAATTAATCTAGGCGCTGTGGCGGCTG 5630
QY 4982 CTGCTGAGGATACGTGGAGGTTACCGGGTGGGATTTCCACTACGTGACGGGCATGA 5041
Db 5631 CTGCTGAGGATACGTGGAGGTTACCGGGTGGGATTTCCACTACGTGACGGGCATGA 5690
QY 5042 CCACCTGACAACTGAAGTCCCGTGTGAGTTCCCGGCGCGCAATTTCTTCAAGAGTGG 5101
Db 5101 CCACCTGACAACTGAAGTCCCGTGTGAGTTCCCGGCGCGCAATTTCTTCAAGAGTGG 5161

Db 5691 CCACCTGACAACTGAAGTCCCGTGTGAGTTCGGCGCGCGCAATTTCTTACAGAACTGG 5750
QY 5102 ATGGGTGCGGTTGCAAGTACGCTCCAGCGGTGCAAAACCCCTCTCTACGAGGAGAGTCA 5161
Db 5751 ATGGGTGCGGTTGCAAGTACGCTCCAGCGGTGCAAAACCCCTCTCTACGAGGAGAGTCA 5810
QY 5162 CATTCTCTGCTCGGGCTCAATCAATACCTGTTGGGTCAAGCTCCCATCGAGCCCGAAC 5221
Db 5811 CATTCTCTGCTCGGGCTCAATCAATACCTGTTGGGTCAAGCTCCCATCGAGCCCGAAC 5870
QY 5222 CGGACGTAGCAGTGTCTCACTCCATCTCACGACCCCTCCACATTAGCGGAGAGCG 5281
Db 5871 CGGACGTAGCAGTGTCTCACTCCATCTCACGACCCCTCCACATTAGCGGAGAGCG 5930
QY 5282 CTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTCTGGCCAGCTCATCAGCTAGCCAGC 5341
Db 5931 CTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTCTGGCCAGCTCATCAGCTAGCCAGC 5990
QY 5342 TGCTCTCGGCTTCTCTTGAAGGCAATGCACTAACCGCTCATGACTCCCGGAGCGTGACC 5401
Db 5991 TGCTCTCGGCTTCTCTTGAAGGCAATGCACTAACCGCTCATGACTCCCGGAGCGTGACC 6050
QY 5402 TCATCGAGCCAACTCTCTGCGCGGAGGATGGCGGGAACATCATCCCGCTGGAGT 5461
Db 6051 TCATCGAGCCAACTCTCTGCGCGGAGGATGGCGGGAACATCATCCCGCTGGAGT 6110
QY 5462 CAGAAATAGGTAAGTAAATTTTGGACTCTTTCGAGCGCTCCAAAGCGAGGAGATGAGA 5521
Db 6111 CAGAAATAGGTAAGTAAATTTTGGACTCTTTCGAGCGCTCCAAAGCGAGGAGATGAGA 6170
QY 5522 GGGAGTATTCGTTCCCGCGGAGATCTTCGCGGAGTCCAGGAAATTCCTCGAGCGATGC 5581
Db 6171 GGGAGTATTCGTTCCCGCGGAGATCTTCGCGGAGTCCAGGAAATTCCTCGAGCGATGC 6230
QY 5582 CCATATGGGACGCGCGGATTAACAACCTCCACTGTTAGAGTCTTGAAGACCGGACT 5641
Db 6231 CCATATGGGACGCGCGGATTAACAACCTCCACTGTTAGAGTCTTGAAGACCGGACT 6290
QY 5642 ACCTCTCTCAGTGGTACAAGGTTGCTTTCGCGCTGCCAAGCGCCCTCCGATACCAC 5701
Db 6291 ACCTCTCTCAGTGGTACAAGGTTGCTTTCGCGCTGCCAAGCGCCCTCCGATACCAC 6350
QY 5702 CTCACGAGGAGAGAGAGCGGTTGCTCTGTCAGAACTACCGTGTCTTCTGCTTGGCGG 5761
Db 6351 CTCACGAGGAGAGAGAGCGGTTGCTCTGTCAGAACTACCGTGTCTTCTGCTTGGCGG 6410
QY 5762 AGCTCGCCACAAAGACCTTCGGCAGCTCCGAACTCGTGGCGGTCGACAGCGGACCGCAA 5821
Db 6411 AGCTCGCCACAAAGACCTTCGGCAGCTCCGAACTCGTGGCGGTCGACAGCGGACCGCAA 6470
QY 5822 CGGCTCTCTGACCGCCCTCCGACGACGCGGATCCGAGTTCGAGTTCGTTACT 5881
Db 6471 CGGCTCTCTGACCGCCCTCCGACGACGCGGATCCGAGTTCGAGTTCGTTACT 6530
QY 5882 CTTCCATGCCCCCTTGAAGGAGCGCGGGGATCCCGATCTCAGCAGCGGCTCTTGGT 5941
Db 6531 CTTCCATGCCCCCTTGAAGGAGCGCGGGGATCCCGATCTCAGCAGCGGCTCTTGGT 6590
QY 5942 CTACCTTAAGCAGGAGGCTAGTGAAGAGCTGCTGCTGCTCGATGTCCTACATGGA 6001
Db 6591 CTACCTTAAGCAGGAGGCTAGTGAAGAGCTGCTGCTGCTCGATGTCCTACATGGA 6061
QY 6002 CAGGCGCTGATCAGCCATGCGTTCGAGGAGAAACCAAGCTGCCATCAATGCACTGA 6061
Db 6651 CAGGCGCTGATCAGCCATGCGTTCGAGGAGAAACCAAGCTGCCATCAATGCACTGA 6710
QY 6062 GCAACTCTTGTCTCGTACCAAACTTGGTCTATGCTAAACATCTCGCAGCGCAAGCC 6121
Db 6711 GCAACTCTTGTCTCGTACCAAACTTGGTCTATGCTAAACATCTCGCAGCGCAAGCC 6770
QY 6122 TCGCGCAGAGAGGCTCACCTTTGACAGCTCGAGTCTTGACGACCACTACCGGAGC 6181
Db 6771 TCGCGCAGAGAGGCTCACCTTTGACAGCTCGAGTCTTGACGACCACTACCGGAGC 6830

Qy	7262	CTCATTTCTTCTCCATCTCTTCTAGCTCAGGAACAACCTTGAAGAGCCCTAGATTGTGAGA	7321
Db	7911	CTCATTTCTTCTCCATCTCTTCTAGCTCAGGAACAACCTTGAAGAGCCCTAGATTGTGAGA	7970
Qy	7322	TCTACGGGGCGCTGTACTCCATTGAGCCACTTGAACCTACCTCAGATCAATCAACGACTCC	7381
Db	7971	TCTACGGGGCGCTGTACTCCATTGAGCCACTTGAACCTACCTCAGATCAATCAACGACTCC	8030
Qy	7382	ATGGCTTTAGGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTT	7441
Db	8031	ACGGCTTTAGGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTT	8090
Qy	7442	CATGCTCAGGAAACTTGGGGTACCGCTTCCGAGTCTGGAGACATCGGGCCAGAGTG	7501
Db	8091	CATGCTCAGGAAACTTGGGGTACCGCTTCCGAGTCTGGAGACATCGGGCCAGAGTG	8150
Qy	7502	TCGGGCTTAGGCTACTGTCAGGGGGGAGGGCTGCCACTTTGTGCAAGTACTCTTCA	7561
Db	8151	TCGGGCTTAGGCTACTGTCAGGGGGGAGGGCTGCCACTTTGTGCAAGTACTCTTCA	8210
Qy	7562	ACTGGGCACTAAGGACCAAGCTCAACTCACTCCAAATCCCGGCTCGTCCAGTTCGATT	7621
Db	8211	ACTGGGCACTAAGGACCAAGCTCAACTCACTCCAAATCCCGGCTCGTCCAGTTCGATT	8270
Qy	7622	TATCCAGCTGGTTCTGTTGCTGGTTACAGCGGGGGAGACATATATACAGCTCTCTCGTG	7681
Db	8271	TATCCAGCTGGTTCTGTTGCTGGTTACAGCGGGGGAGACATATATACAGCTCTCTCGTG	8330
Qy	7682	CCGAGCCCGCTGGTTCACTGCTGCTACTCTCTACTTTCTGAGGGGTAGGCACTCTATC	7741
Db	8331	CCGAGCCCGCTGGTTCACTGCTGCTACTCTCTACTTTCTGAGGGGTAGGCACTCTATC	8390
Qy	7742	TACTCCCCAACCGATGAACGGGAGCTAAACATCCAGGCAATAGGCCATCTGTTTTT	7801
Db	8391	TACTCCCCAACCGATGAACGGGAGCTAAACATCCAGGCAATAGGCCATCTGTTTTT	8450
Qy	7802	TTCCCTT	7861
Db	8451	TTCCCTT	8510
Qy	7862	TTTTCTCTTT	7921
Db	8511	TTTTCTCTTT	8570
Qy	7922	AGCTGTGAAGGTCCTGAGCGCTTCACTGAGAGAGTCTGATCTAGCTAGTCAACGGCT	7981
Db	8571	AGCTGTGAAGGTCCTGAGCGCTTCACTGAGAGAGTCTGATCTAGCTAGTCAACGGCT	8630
Qy	7982	GATCAAGT 7989	
Db	8631	GATCAAGT 8638	
RESULT 10			
US-10-029-907-7			
Sequence 7, Application US/10029907			
Patent No. 6706874			
GENERAL INFORMATION:			
APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.			
TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM			
TITLE OF INVENTION: HEPATITIS C VIRUS			
FILE REFERENCE: 13/083			
CURRENT APPLICATION NUMBER: US/10/029,907			
CURRENT FILING DATE: 2001-12-21			
PRIOR APPLICATION NUMBER: 60/257,857			
PRIOR FILING DATE: 2000-12-22			
NUMBER OF SEQ ID NOS: 25			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 7			
LENGTH: 8638			
TYPE: DNA			
ORGANISM: HCV			
FEATURE:			

Qy	6182	TGCTCAAGAGATGAAGCGAAGCGTCCACAGTTAAGGCTAAATCTTATCCGTGGAGG	6241
Db	6831	TGCTCAAGAGATGAAGCGAAGCGTCCACAGTTAAGGCTAAATCTTATCCGTGGAGG	6890
Qy	6242	AAGCTCTGAAGTGAAGCGGCGGCAATTCGGCCAGATCTAAATTTGGCTATGGGGCAAGG	6301
Db	6891	AAGCTCTGAAGTGAAGCGGCGGCAATTCGGCCAGATCTAAATTTGGCTATGGGGCAAGG	6950
Qy	6302	AGTCCGGAACCTATCCAGCAAGCGGTTAAACACATCCGCTCCGTGTGGAAAGCACTTGC	6361
Db	6951	AGTCCGGAACCTATCCAGCAAGCGGTTAAACACATCCGCTCCGTGTGGAAAGCACTTGC	7010
Qy	6362	TGGAAGACACTGAGACACCAATATGACACACCAATATGCGCAAAATAGGTTTCTGCG	6421
Db	7011	TGGAAGACACTGAGACACCAATATGACACACCAATATGCGCAAAATAGGTTTCTGCG	7070
Qy	6422	TCCAAACAGAGAGGGGGCGGCAAGCCAGCTCGCCTTATCGTATTCACAGATTTGGGGG	6481
Db	7071	TCCAAACAGAGAGGGGGCGGCAAGCCAGCTCGCCTTATCGTATTCACAGATTTGGGGG	7130
Qy	6482	TTCTGTGTGCGGAAATAGGCTTTACGATGTGCTCTCCACCTCCCTCAGGCCGTGA	6541
Db	7131	TTCTGTGTGCGGAAATAGGCTTTACGATGTGCTCTCCACCTCCCTCAGGCCGTGA	7190
Qy	6542	TGGGCTCTTTCATACGATTCGAATATCTCTCTGGAAGCGGTCGAGTTCCTGTTGAATG	6601
Db	7191	TGGGCTCTTTCATACGATTCGAATATCTCTCTGGAAGCGGTCGAGTTCCTGTTGAATG	7250
Qy	6602	CCTGGAAGCGAAGATGCCCTATGGCTTCCATATGACACCCGCTGTTTGACTCAA	6661
Db	7251	CCTGGAAGCGAAGATGCCCTATGGCTTCCATATGACACCCGCTGTTTGACTCAA	7310
Qy	6662	CGTCACTGAGATGACATCCGTTGTGAGGAGTCAATCTACCAATGTGTGACTTGGCCC	6721
Db	7311	CGTCACTGAGATGACATCCGTTGTGAGGAGTCAATCTACCAATGTGTGACTTGGCCC	7370
Qy	6722	CCGAAGCAGACAGGCTAAGTGTCTCAGAGCGGCTTACATCGGGGGCCCCCTGA	6781
Db	7371	CCGAAGCAGACAGGCTAAGTGTCTCAGAGCGGCTTACATCGGGGGCCCCCTGA	7430
Qy	6782	CTAATTTTAAAGGCGAAGCTCGGCTATCCCGTTCGCGGCGGAGGCTGACTGACGA	6841
Db	7431	CTAATTTTAAAGGCGAAGCTCGGCTATCCCGTTCGCGGCGGAGGCTGACTGACGA	7490
Qy	6842	CCAGTCCGGTAAATACCTCACAATGTTACTTGAAGGCGCTGCGGCTGTCGAGCTGCGA	6901
Db	7491	CCAGTCCGGTAAATACCTCACAATGTTACTTGAAGGCGCTGCGGCTGTCGAGCTGCGA	7550
Qy	6902	AGCTCCAGGACTGACAGATGCTCGTATCGGAGAGGACCTTGTGTTATCTGTGAAGCG	6961
Db	7551	AGCTCCAGGACTGACAGATGCTCGTATCGGAGAGGACCTTGTGTTATCTGTGAAGCG	7610
Qy	6962	CGGGACCCAGAGAGGAGCGAGCTTACGGGCTTCAAGGAGGCTATGACTAGATACT	7021
Db	7611	CGGGACCCAGAGAGGAGCGAGCTTACGGGCTTCAAGGAGGCTATGACTAGATACT	7670
Qy	7022	CTGCCCCCTGGGACCCGCCAAACAGAAATACGATGAGTGTGATAACATCATGCT	7081
Db	7671	CTGCCCCCTGGGACCCGCCAAACAGAAATACGATGAGTGTGATAACATCATGCT	7730
Qy	7082	CCTCAATGTGTGAGTCCGGACGATGATCTGGCAAGGCTGACTATCTCACCCGTG	7141
Db	7731	CCTCAATGTGTGAGTCCGGACGATGATCTGGCAAGGCTGACTATCTCACCCGTG	7790
Qy	7142	ACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7201
Db	7791	ACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT	7850
Qy	7202	CCTGGCTAGGCAACATCATATGATATGGCCCACTTGTGGCAAGGATGATCTGATCA	7261
Db	7851	CCTGGCTAGGCAACATCATATGATATGGCCCACTTGTGGCAAGGATGATCTGATCA	7910

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; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-029-907-7

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Query Match	90.7%	Score 7249.8;	DB 4;	Length 8638;
Best Local Similarity	92.0%	Score 7249.8;	DB 4;	Length 8638;

	Local similarity	92.0%	0	Mismatches	17	Indels	671	Gaps	3
	Matches	7961	Conservative						
QY	1	GCAGCCCCGATTTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAAC	CTACTG	60					
Db	1	GCAGCCCCGATTTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAAC	CTACTG	60					
QY	61	TCATTACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTG	CAGCTCCAGGAC	120					
Db	61	TCATTACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTG	CAGCTCCAGGAC	120					
QY	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGAACCGGTGAGTACACCGAA	TGCGAG	180					
Db	121	CCCCCTCCCGGAGAGCCATAGTGGTCTGCGAACCGGTGAGTACACCGAA	TGCGAG	180					
QY	181	GACGACCGGGTCTTTCTTGGATCAACCCCGCTCAATGCTGGAGATTGGG	CGTGC	240					
Db	181	GACGACCGGGTCTTTCTTGGATCAACCCCGCTCAATGCTGGAGATTGGG	CGTGC	240					
QY	241	GGAGACTGCTAGCCGAGTGTGGTTCGCGAAAGCGCTTGTGTACTGCTG	ATAGG	300					
Db	241	GGAGACTGCTAGCCGAGTGTGGTTCGCGAAAGCGCTTGTGTACTGCTG	ATAGG	300					
QY	301	GTGCTTGGAGTGGCCCCGGGAGGTCTCGTAGACCGTGCACATGAGCA	CGAATCTTAAC	360					
Db	301	GTGCTTGGAGTGGCCCCGGGAGGTCTCGTAGACCGTGCACATGAGCA	CGAATCTTAAC	360					
QY	361	CTCAAGAAAAACCAAGAGGCGGCCATGATTGAACAAAGATTGCACGAG	GTTC	420					
Db	361	CTCAAGAAAAACCAAGAGGCGGCCATGATTGAACAAAGATTGCACGAG	GTTC	420					
QY	421	CGGCGCTTGGGTGGAGAGGCTATTGGCTACACTGGGCAACAAGATG	ATGCA	480					
Db	421	CGGCGCTTGGGTGGAGAGGCTATTGGCTACACTGGGCAACAAGATG	ATGCA	480					
QY	481	CTGATGCGCGGTTCCTCCGCTCTGCAGCGCAGGGCGCCCGGTTCTTT	TGTCAAGACG	540					
Db	481	CTGATGCGCGGTTCCTCCGCTCTGCAGCGCAGGGCGCCCGGTTCTTT	TGTCAAGACG	540					
QY	541	ACCTGTCGGGTGCCCTCAATGAACCTGAGGA	CGAGGACGCGGCTATCGTGGCTGGCCA	600					
Db	541	ACCTGTCGGGTGCCCTCAATGAACCTGAGGA	CGAGGACGCGGCTATCGTGGCTGGCCA	600					
QY	601	CGACGGGCTTCCTTGGCAGCTGTCTCGACGCTTGCTACACGCTTGCT	CACTCACTGCTCGCGAGA	720					
Db	601	CGACGGGCTTCCTTGGCAGCTGTCTCGACGCTTGCTACACGCTTGCT	CACTCACTGCTCGCGAGA	720					
QY	661	TGCTATTGGGCGAAGTGC	CGGGCGAGATCTCCTGTCTCACTCCTGCTCGCGAGA	780					
Db	661	TGCTATTGGGCGAAGTGC	CGGGCGAGATCTCCTGTCTCACTCCTGCTCGCGAGA	780					
QY	721	AAGTATCCATCATGCTGTGATCAATGCGCGGCTCGATACGCTTGCT	CGCTACCTGCTCGCGAGA	840					
Db	721	AAGTATCCATCATGCTGTGATCAATGCGCGGCTCGATACGCTTGCT	CGCTACCTGCTCGCGAGA	840					
QY	781	CATTTCACACCAAGCGAAATCCGATCGACGAGCACGTACTCGGATG	GAAGCCGGTC	840					
Db	781	CATTTCACACCAAGCGAAATCCGATCGACGAGCACGTACTCGGATG	GAAGCCGGTC	840					
QY	841	TTGTCCATCAGATGATCTGGACGAGAGCATCAGGGCTCGGCCACCG	CAACTGTTCC	900					
Db	841	TTGTCCATCAGATGATCTGGACGAGAGCATCAGGGCTCGGCCACCG	CAACTGTTCC	900					
QY	901	CCAGGCTCAAGCGCGCATGCCCAGCGCGAGGATCTCGTCAACCAT	GGCGATGCCT	960					
Db	901	CCAGGCTCAAGCGCGCATGCCCAGCGCGAGGATCTCGTCAACCAT	GGCGATGCCT	960					
QY	961	GCTTGGCGAATATCATGTTGGAAATGGCCGCTTTCTGGATTATCAT	CGATGTGGCGGGC	1020					

Tue Nov 2 14:02:16 2004

Db	2030	TTTACATCAAAATCTTGCTGCCATATCTCGTCCACTCATGGTCTCCAGGCTGGT	2089
QY	1804	-----	1803
Db	2090	ATAACAAAGTCCGTACTTTCGTGCGCAGCAGGGCTCATTCGTGATCATGCTGGTG	2149
QY	1804	-----	1803
Db	2150	CGGAAGTTGCTGGGGTCATTATGTATCCAAATGGCTCTCATGAAGTTGGCCGCACTGACA	2209
QY	1804	-----	1803
Db	2210	GGTACGTACGTTTANGACCATCTCACCCCACTGCGGACTGGGCCCAACGGGGCCTTACGA	2269
QY	1804	-----	1803
Db	2270	GACCTTGGCGTGCAGTTGAGCCCGTGGTCTTCTCTGATATGAGACCAAGGTTATACCC	2329
QY	1804	-----	1803
Db	2330	TGGGGGCGACACACCGCGCGTGTGGGACATCATCTTGGGCGCTGCCGCTCTCGGCCGC	2389
QY	1804	-----	1803
Db	2390	AGGGGAGGGAGATACATCTGGGACCGGCGACAGAGCCCTTGAAGGACAGGGTGGGACTC	2449
QY	1804	-----	1803
Db	2450	CTCGGCTATTAGCGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCAC	2509
QY	1861	AGCCTCAGCGCGGACAGGAACAGAGTGCAGGGGAGGCTCCAAAGTGGCTCCACACGCA	1920
Db	2510	AGCCTCAGCGCGGACAGGAACAGAGTGCAGGGGAGGCTCCAAAGTGGCTCCACACGCA	2569
QY	1921	ACAAATCTTCTCGGACCTCGGTCAAATGGCGTGTGTGGACTGTCTATCATGGTGCC	1980
Db	2570	ACAAATCTTCTCGGACCTCGGTCAAATGGCGTGTGTGGACTGTCTATCATGGTGCC	2629
QY	1981	GGCTCAAGAGCCCTTGGCGGCCAAAGGCGCAATCAACCAAAATGACCAATGTGGAC	2040
Db	2630	GGCTCAAGAGCCCTTGGCGGCCAAAGGCGCAATCAACCAAAATGACCAATGTGGAC	2689
QY	2041	CAGACCTCGTGGTGGAGAGCGCCCGCGGGCGCTTCTTGACACCATGACCTGC	2100
Db	2690	CAGACCTCGTGGTGGAGAGCGCCCGCGGGCGCTTCTTGACACCATGACCTGC	2749
QY	2101	GGCAGCTCGGACCTTACTTGTGTACAGGAGCATGCCATGTCAATTCGGTGGCGCGGG	2160
Db	2750	GGCAGCTCGGACCTTACTTGTGTACAGGAGCATGCCATGTCAATTCGGTGGCGCGGG	2809
QY	2161	GGCGACAGCAGGGGGAGCTACTCTCCCGAGCGCGCTCTCTAATTGAAGGCTCTTCG	2220
Db	2810	GGCGACAGCAGGGGGAGCTACTCTCCCGAGCGCGCTCTCTAATTGAAGGCTCTTCG	2869
QY	2221	GGCGGTGCACTGTCTGCCCCCTCGGGACGCTGTGGGCACTCTTCGGGCTGCCGTGTGC	2280
Db	2870	GGCGGTGCACTGTCTGCCCCCTCGGGACGCTGTGGGCACTCTTCGGGCTGCCGTGTGC	2929
QY	2281	ACCGAGGGGTTGCGAAGCGGTGGACTTTGTATACCGGTGAGTCTATGGAACCACTATG	2340
Db	2930	ACCGAGGGGTTGCGAAGCGGTGGACTTTGTATACCGGTGAGTCTATGGAACCACTATG	2989
QY	2341	CGGTCCCGGCTTTCACGCAAACTCGTCCCTCGCGCGGTACCGAGACATTCAGGTG	2400
Db	2990	CGGTCCCGGCTTTCACGCAAACTCGTCCCTCGCGCGGTACCGAGACATTCAGGTG	3049
QY	2401	GCCCATCTACAGCCCTTACTGTAGCGGCAAGAGCACTAAGTGGCGGCTGGTATGCA	2460
Db	3050	GCCCATCTACAGCCCTTACTGTAGCGGCAAGAGCACTAAGTGGCGGCTGGTATGCA	3109
QY	2461	GCCCAAGGTTAAGGTTCTTCTCTGAACCGGTCCGTGGCGGCAACCTAGGTTTCGG	2520
Db	3110	GCCCAAGGTTAAGGTTCTTCTCTGAACCGGTCCGTGGCGGCAACCTAGGTTTCGG	3169
QY	2521	GGTATATGTCTAAGGCACTGGTATCGACCTAACATCAGAACCGGGTAAAGGACCATC	2580
Db	3170	GGTATATGTCTAAGGCACTGGTATCGACCTAACATCAGAACCGGGTAAAGGACCATC	3229
QY	2581	ACCAGGGTGGCCCATCAGCTACTCCACCTATGGCAAGTTTCTTGGCCAGCGGTGGTGC	2640
Db	3230	ACCAGGGTGGCCCATCAGCTACTCCACCTATGGCAAGTTTCTTGGCCAGCGGTGGTGC	3289
QY	2641	TCCTGGGGCGCTATGACATCATATATGTGATGATGCTCACTCACTCACTCGACCAT	2700
Db	3290	TCCTGGGGCGCTATGACATCATATATGTGATGATGCTCACTCACTCACTCGACCAT	3349
QY	2701	ATCTGGGGCATCGGCAAGTCTTGACCAAGCGGAGACGCTGGAGCGGACTCTGCTGCTG	2760
Db	3350	ATCTGGGGCATCGGCAAGTCTTGACCAAGCGGAGACGCTGGAGCGGACTCTGCTGCTG	3409
QY	2761	CTCGCCACCGCTACCGCTCGGGATCGGTCAACCGTCCCATCATCCAAACATCGAGAGGTG	2820
Db	3410	CTCGCCACCGCTACCGCTCGGGATCGGTCAACCGTCCCATCATCCAAACATCGAGAGGTG	3469
QY	2821	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCAATCCCATCGGACCATC	2880
Db	3470	GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCAATCCCATCGGACCATC	3529
QY	2881	AAGGGGGAGGAGCACTCATTTTCTGCCATTCCAAGAGAAATGTGATGACTCGCCGCG	2940
Db	3530	AAGGGGGAGGAGCACTCATTTTCTGCCATTCCAAGAGAAATGTGATGACTCGCCGCG	3589
QY	2941	AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTTACCGGGGCTTTGATGATCGCTC	3000
Db	3590	AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTTACCGGGGCTTTGATGATCGCTC	3649
QY	3001	ATACAACTAGCGGAGACGCTCATTTCTGTAGCAACGAGCGCTTAATGACGGGCTTTACC	3060
Db	3650	ATACAACTAGCGGAGACGCTCATTTCTGTAGCAACGAGCGCTTAATGACGGGCTTTACC	3709
QY	3061	GGGATTTGACTCAGTGTGACTGCAATACATGTGTACCCAGACAGTGTGACTTCAGC	3120
Db	3710	GGGATTTGACTCAGTGTGACTGCAATACATGTGTACCCAGACAGTGTGACTTCAGC	3769
QY	3121	CTGGACCGACCTTACCATTTGAGACGACGACCTGTGCCAAGACGCGGTGTACGCTCG	3180
Db	3770	CTGGACCGACCTTACCATTTGAGACGACGACCTGTGCCAAGACGCGGTGTACGCTCG	3829
QY	3181	CAGCGCGAGGAGGAGTGTGAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3240
Db	3830	CAGCGCGAGGAGGAGTGTGAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA	3889
QY	3241	GAAAGGCTCGGGCATGTTGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT	3300
Db	3890	GAAAGGCTCGGGCATGTTGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT	3949
QY	3301	GCTTGTAGAGCTCAGCGCCCGCGAGACCTCAGTTAGGTTTGGGGCTTACCTAAACACA	3360
Db	3950	GCTTGTAGAGCTCAGCGCCCGCGAGACCTCAGTTAGGTTTGGGGCTTACCTAAACACA	4009
QY	3361	CCAGGTTTCCCGTCTGCGGAGGACCATCTGGAGTTCCTGGAGAGCGCTTTTACAGGCTC	3420
Db	4010	CCAGGTTTCCCGTCTGCGGAGGACCATCTGGAGTTCCTGGAGAGCGCTTTTACAGGCTC	4069
QY	3421	ACCACATAGACGCGCCATTTCTTGTCCGAGCTTAAGCAGCAGGAGACAACTTCCCTAC	3480
Db	4070	ACCACATAGACGCGCCATTTCTTGTCCGAGCTTAAGCAGCAGGAGACAACTTCCCTAC	4129
QY	3481	CTGCTAGCATACAGGCTACGCTGTGCGCGGAGGCTCAGGCTCCACTCGTGGGAC	3540
Db	4130	CTGCTAGCATACAGGCTACGCTGTGCGCGGAGGCTCAGGCTCCACTCGTGGGAC	4189
QY	3541	CAAAATGTGAAGTGTCTCATACGCTTAAAGCTTACGCTGACGCGGCAACGCGCTGCTG	3600
Db	4190	CAAAATGTGAAGTGTCTCATACGCTTAAAGCTTACGCTGACGCGGCAACGCGCTGCTG	4249

Db	6410	GAGCTCGCCACAAAGACCTTCGGCAGCTCCGAATCGTTCGGCCGTCGACAGCGGCACGCA	6469	Qy	6901	AAGCTCCAGGACTGACGATGCTCGTATGCGGAGGACCTTGCTGTTATCTGTGAAGC	6960
Qy	5821	ACGGCTCTCTCGTACCAAGCCTTCGACGACGCGGAGCTCCGAGCTTGAGTCGTAC	5880	Db	7550	AAGCTCCAGGACTGACGATGCTCGTATGCGGAGGACCTTGCTGTTATCTGTGAAGC	7609
Db	6470	ACGGCTCTCTCGTACCAAGCCTTCGACGACGCGGAGCTCCGAGCTTGAGTCGTAC	6529	Qy	6961	GCGGGACCCAAAGAGGACGAGCGGAGCTTACGGGCTTCACGGAGGCTATGACTAGATC	7020
Qy	5881	TCCTCCATGCCCCCTTTAGGGGAGCGGGGGATCCGGATCTCAGACGAGGCTTTGG	5940	Db	7610	GCGGGACCCAAAGAGGACGAGCGGAGCTTACGGGCTTCACGGAGGCTATGACTAGATC	7669
Db	6530	TCCTCCATGCCCCCTTTAGGGGAGCGGGGGATCCGGATCTCAGGACGAGGCTTTGG	6589	Qy	7021	TCCTCCATGCTCAGTCGCGCACGATGATCTGCGGAGGCTTGGAGTTGATACATCATC	7080
Qy	5941	TCCTCCATGCCCCCTTTAGGGGAGCGGGGGATCCGGATCTCAGGACGAGGCTTTGG	6000	Db	7670	TCCTCCATGCTCAGTCGCGCACGATGATCTGCGGAGGCTTGGAGTTGATACATCATC	7729
Db	6590	TCCTCCATGCCCCCTTTAGGGGAGCGGGGGATCCGGATCTCAGGACGAGGCTTTGG	6649	Qy	7081	TCCTCCATGCTCAGTCGCGCACGATGATCTGCGGAGGCTTGGAGTTGATACATCATC	7140
Qy	6001	ACAGGCGGCTGATCAGCGCATCGCTGCGGAGGAAACCAAGTCGCCATCAATGCACTG	6060	Db	7730	TCCTCCATGCTCAGTCGCGCACGATGATCTGCGGAGGCTTGGAGTTGATACATCATC	7789
Db	6650	ACAGGCGGCTGATCAGCGCATCGCTGCGGAGGAAACCAAGTCGCCATCAATGCACTG	6709	Qy	7141	GAACCCACACCCCTTCGCGGGCTGCTGGGAGACAGCTAGACACACTCCAGTCAAT	7200
Qy	6061	AGCAACTCTTTGCTCCGTCACCAAACTTGGTCTATGCTACACATCTCGCAGCGAAGC	6120	Db	7790	GAACCCACACCCCTTCGCGGGCTGCTGGGAGACAGCTAGACACACTCCAGTCAAT	7849
Db	6710	AGCAACTCTTTGCTCCGTCACCAAACTTGGTCTATGCTACACATCTCGCAGCGAAGC	6769	Qy	7201	TCCTGGCTAGGCAACATCATCATGATGATGCGGCCACCTTGTGGCAAGGATGATCTGATG	7260
Qy	6121	CTGGGAGAGAAAGTCACTTTGACAGACTGACAGTCTCGGAGCAACACTACCGGGAC	6180	Db	7850	TCCTGGCTAGGCAACATCATCATGATGATGCGGCCACCTTGTGGCAAGGATGATCTGATG	7909
Db	6770	CTGGGAGAGAAAGTCACTTTGACAGACTGACAGTCTCGGAGCAACACTACCGGGAC	6829	Qy	7261	ACTCAATTTCTTCCATCTCTTAGCTCAGGAACTTCAAAAAGCCCTAGATTTGTCAG	7320
Qy	6181	GTGCTCAAGGAGATGAAGGGAAGGCGTCCACAGTTAAGGCTTAACTTTATCTGCGGAG	6240	Db	7910	ACTCAATTTCTTCCATCTCTTAGCTCAGGAACTTCAAAAAGCCCTAGATTTGTCAG	7969
Db	6830	GTGCTCAAGGAGATGAAGGGAAGGCGTCCACAGTTAAGGCTTAACTTTATCTGCGGAG	6889	Qy	7321	ATCTACGGGCGCTTACTCCATTTAGCCACTTGACCTACTCAGATCAATTCACGACTC	7380
Qy	6241	GAAGCTGTAGCTGACGCCGCCACATTCGGCGAGATCTAAATTTGGCTATGGGGCAAG	6300	Db	7970	ATCTACGGGCGCTTACTCCATTTAGCCACTTGACCTACTCAGATCAATTCACGACTC	8029
Db	6890	GAAGCTGTAGCTGACGCCGCCACATTCGGCGAGATCTAAATTTGGCTATGGGGCAAG	6949	Qy	7381	CATGGCTTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGCTGCT	7440
Qy	6301	GAAGCTGTAGCTGACGCCGCCACATTCGGCGAGATCTAAATTTGGCTATGGGGCAAG	6360	Db	8030	CATGGCTTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGCTGCT	8089
Db	6950	GAAGCTGTAGCTGACGCCGCCACATTCGGCGAGATCTAAATTTGGCTATGGGGCAAG	7009	Qy	7441	TCATGGCTCAGGAACTTGGGGTACCGGCTTGGAGTCTGGAGTCTGGAGACATCGGGCCAGAACT	7500
Qy	6361	CTGGAAGACACTGACACCAATTTGACACCACTTACATGATGGAACCAATTTGAGGTTTCTGC	6420	Db	8090	TCATGGCTCAGGAACTTGGGGTACCGGCTTGGAGTCTGGAGTCTGGAGACATCGGGCCAGAACT	8149
Db	7010	CTGGAAGACACTGACACCAATTTGACACCACTTACATGATGGAACCAATTTGAGGTTTCTGC	7069	Qy	7501	GTCCGCGTACGCTACTGTCACGGGGGAGGCTGCGCACTGTTGGCAAGTACTCTCTTC	7560
Qy	6421	GTCCAAACAGAGAGGGGGCGGAGCGGCTTATCGTATTCAGATTTGGG	6480	Db	8150	GTCCGCGTACGCTACTGTCACGGGGGAGGCTGCGCACTGTTGGCAAGTACTCTCTTC	8209
Db	7070	GTCCAAACAGAGAGGGGGCGGAGCGGCTTATCGTATTCAGATTTGGG	7129	Qy	7561	AACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGAT	7620
Qy	6481	GTTCGTGTGCGAGAAATGCCCCCTTTACGATGTTGCTCCACCCCTCCCTCAGGCGGTG	6540	Db	8210	AACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGAT	8269
Db	7130	GTTCGTGTGCGAGAAATGCCCCCTTTACGATGTTGCTCCACCCCTCCCTCAGGCGGTG	7189	Qy	7621	AACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGAT	7680
Qy	6541	ATGGGCTCTTCAACGATTTCAATATCTCTCTGAGACAGCGGTCGAGTTCTGTTGAAT	6600	Db	8270	AACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGAT	8329
Db	7190	ATGGGCTCTTCAACGATTTCAATATCTCTCTGAGACAGCGGTCGAGTTCTGTTGAAT	7249	Qy	7681	GTCCGAGCCCGCTGTTGATGTTGCTGCTTACTCTTCTGTTAGGGTAGGCACTAT	7740
Qy	6601	GTCTGAAAGCGAAGAAATGCCCTTATGGCTTCGATATGACACCCGCTGTTTGAATCA	6660	Db	8330	GTCCGAGCCCGCTGTTGATGTTGCTGCTTACTCTTCTGTTAGGGTAGGCACTAT	8389
Db	7250	GTCTGAAAGCGAAGAAATGCCCTTATGGCTTCGATATGACACCCGCTGTTTGAATCA	7309	Qy	7741	CTACTCCCCAACCGATGAAACCGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	7800
Qy	6661	ACGGTCACTCAGAAATGACATCCGCTGTTGAGGAGTCAATCTACCAATGTTGATGAGCC	6720	Db	8390	CTACTCCCCAACCGATGAAACCGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT	8449
Db	7310	ACGGTCACTCAGAAATGACATCCGCTGTTGAGGAGTCAATCTACCAATGTTGATGAGCC	7369	Qy	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Qy	6721	CCGAGCCAGACAGGCGCATAGGTCCTCAGAGCGGCTTACATCGGGGGCCCCCTG	6780	Db	8450	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8509
Db	7370	CCGAGCCAGACAGGCGCATAGGTCCTCAGAGCGGCTTACATCGGGGGCCCCCTG	7429	Qy	7861	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Qy	6781	ACTAATTTCTAAGGGGAGAACTCGGCTATCGCGGTGCGCGGAGCGGTGACTGACG	6840	Db	8510	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8569
Db	7430	ACTAATTTCTAAGGGGAGAACTCGGCTATCGCGGTGCGCGGAGCGGTGACTGACG	7489	Qy	7921	TAGCTGTGAAGGTCCTGTAGCGGCTGATCTGACAGAGTGTGATGACTGCTCTCTGC	7980
Qy	6841	ACCAGCTCGGCTAATACCTTACATGTTACTTTGAGGCGCGCTGCGGCTGTCGAGTGGC	6900	Db	8570	TAGCTGTGAAGGTCCTGTAGCGGCTGATCTGACAGAGTGTGATGACTGCTCTCTGC	8629
Db	7490	ACCAGCTCGGCTAATACCTTACATGTTACTTTGAGGCGCGCTGCGGCTGTCGAGTGGC	7549				

QY 7981 AGATCAAGT 7989
Db 8630 AGATCAAGT 8638

RESULT 11

US-10-029-907-25
; Sequence 25, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; PRIORITY FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIORITY FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)....(8407)
US-10-029-907-25

Query Match
Best Local Similarity 90.7%; Score 7248.8; DB 4; Length 8638;
Matches 7960; Conservative 0; Mismatches 17; Indels 671; Gaps 3;
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Db 2 CCAGCCCCGATGGGGGACACTCCACCAATAGATCACTCCCTGTGAGAACTACTGT 61
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Db 62 CTTCACGAGAAAGCTCTAGCCATGGCGTTAGTATGATGTGTCAGAGCTCCAGGACC 121
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Db 182 ACGACCGGCTCTTTCTTGATCAACCGCTCAATGCTGAGATTTGGGCGTCCCGCCG 241
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QY 302 TGTGTGAGTGTCCCGGAGGCTCTGTAGACCGTGCACCATGAGCAGAACTCTAAAC 361
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Db 1490 GCAGGCGAGCGGAAACCTGCGCGGCGGAAACCTGCGCGCTTCTGCTTTGA 1550
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Db 1550 AAGATACACTGCAAGGCGGCAACCTGCGCGGCGGAAACCTGCGCGCTTCTGCTTTGA 1610
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Db 1610 AAGAGTCAATGGCTTCTCAAGCGTATCAACAAAGGCGGCTGAGGATGCGCGAGG 1670
QY 1670 TACCCCAATGATGGATCTGATCTGCGGCGCTGCGGCGCATGCTTTTACATGCTTTAGT 1729

Db	1671	TACCCCAATGATGGATCTGATCTGGGGCTCGGTGCACATGCTTACATGCTTTAGT	1730	2751	GGAGTCGGACCTTTACTTGTGTCAAGACATGCCGATGTCATTCCTGGGTGCGCGCGGG	2810
Qy	1730	CGAGGTTAAAGAAACGCTAGGCCCCCGAACACACGGGACGCTGTTTCTTTGAAAAC	1789	2162	CGACAGCAGGGGAGCCCTACTCTCCCAAGCCCGTCTCTACTTTGAAGGCTCTTCGG	2221
Db	1731	CGAGGTTAAAGAAACGCTAGGCCCCCGAACACACGGGACGCTGTTTCTTTGAAAAC	1790	2811	GGACAGCAGGGGAGCCCTACTCTCCCAAGCCCGTCTCTACTTTGAAGGCTCTTCGG	2870
Qy	1790	ACGATAATACCATG-----	1803	2222	GGGTGCCATGCTCTGCCCCCTCGGGGACGCTGTGGGCACTTTTGGGGCTGCGGTGTGCA	2281
Db	1791	ACGATAATACCATGACCGGGAGATGGCAGCATCGTGCAGGCGCGGTTTTCGTAGGTC	1850	2871	GGGTGCCATGCTCTGCCCCCTCGGGGACGCTGTGGGCACTTTTGGGGCTGCGGTGTGCA	2930
Qy	1804	-----	1803	2282	CCGAGGGGTTCCGAAGCGGTGGACTTTGTATCCCGTTCAGTCTATGGAACCACTATGC	2341
Db	1851	TGATACTCTTGACCTTGTCAACGCACTATAAGCTGTTCTCGTAGGCTCATATGCTGT	1910	2931	CCGAGGGGTTCCGAAGCGGTGGACTTTGTATCCCGTTCAGTCTATGGAACCACTATGC	2990
Qy	1804	-----	1803	2342	GGTCCCGGCTTTACGACAACTCGTCCCTCCCGCCGTACCGCAGACATTCACAGTGG	2401
Db	1911	TACATAATTTATCACAGGGCGAGGCACACTTGCAGTGTGGATCCCGCCCTCAACG	1970	2991	GGTCCCGGCTTTACGACAACTCGTCCCTCCCGCCGTACCGCAGACATTCACAGTGG	3050
Qy	1804	-----	1803	2402	CCCATCTACGCGCCCTACTCTGGTAGCGCAAGAGCACTAAGTGCCTGCTGCGTATGCAG	2461
Db	1971	TTCCGGGGGCGCGATCGCGTATCTCTCCTCACTCGTGGCGATCCACCGAGCTAATCT	2030	3051	CCCATCTACGCGCCCTACTCTGGTAGCGCAAGAGCACTAAGTGCCTGCTGCGTATGCAG	3110
Qy	1804	-----	1803	2462	CCCAAGGTATAGGTGCTTGTCTGAAACCCGCTCGGTGCGCCGCACTTCTAGGTTTCGGG	2521
Db	2031	TTACCATCACCAAAUCTTGCTCGCCATCTCGGTCCACTCATGCTGCTCCAGGCTGTA	2090	3111	CCCAAGGTATAGGTGCTTGTCTGAAACCCGCTCGGTGCGCCGCACTTCTAGGTTTCGGG	3170
Qy	1804	-----	1803	2522	CGTATATGTCTAAGGCACATGCTATCGACCTTAACATCAGAACCGGGTAAGGACCATCA	2581
Db	2091	TAACCAAGTGCCGTACTTCTGTGCGGCACACGGGCTCATTCGTCATGATGCTGTGC	2150	3171	CGTATATGTCTAAGGCACATGCTATCGACCTTAACATCAGAACCGGGTAAGGACCATCA	3230
Qy	1804	-----	1803	2582	CCAGGGTGCCCCCATCAGTACTCCACCTATGCAAGTTTCTTCCGACGGTGGTGTCT	2641
Db	2151	GGAAAGTTGCTGGGGTCAATATGTCCAAATGGCTCTCATGAAGTTGGCCGCACTGACAG	2210	3231	CCAGGGTGCCCCCATCAGTACTCCACCTATGCAAGTTTCTTCCGACGGTGGTGTCT	3290
Qy	1804	-----	1803	2642	CTGGGGCGCTATGACATCATATATGTGATGCTCCACTCAACTGACCTGACCCACTA	2701
Db	2211	GTACGTAGTTTATGACCATCTACCCCACTGCGGACTGGGCCACCGGGCCCTACGAG	2270	3291	CTGGGGCGCTATGACATCATATATGTGATGCTCCACTCAACTGACCTGACCCACTA	3350
Qy	1804	-----	1803	2702	TCCTGGGCATCGGCACAGTCTCTGACCAAGCGGACGCTGGAGCGGCACTCGTGTGC	2761
Db	2271	ACCTTGCGGTGGCAGTTGAGCCCGTCTGTTCTCTGTATGAGACCAAGGTTATCACT	2330	3351	TCCTGGGCATCGGCACAGTCTCTGACCAAGCGGACGCTGGAGCGGCACTCGTGTGC	3410
Qy	1804	-----	1803	2762	TCGCCACCGCTACCGCTCCGGGATCGGTCACTGCGCACATCCAAATCATCGAGAGGTGG	2821
Db	2331	GGGGGCGAGACACCGCGGCTGTGGGACATCATCTTGGGCTGCGCGTCCCGCCGCA	2390	3411	TCGCCACCGCTACCGCTCCGGGATCGGTCACTGCGCACATCCAAATCATCGAGAGGTGG	3470
Qy	1804	-----	1803	2822	CTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATTCGAGACCATCA	2881
Db	2391	GGGGAGGAGATACATCTGGGACCGGCAGACAGCTTTGAAGGGCAGGGTGGGACTCC	2450	3471	CTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATTCGAGACCATCA	3530
Qy	1804	-----	1803	2882	AGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAATAATGTGATGAGCTCGCGCGA	2941
Db	2451	TCGGGCTTATTACGGCTACTCCCAACAGACGAGGCTACTTGGCTGCATCATCTA	1861	3531	AGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAATAATGTGATGAGCTCGCGCGA	3590
Qy	1862	GCTCAGCGCGGACAGAACAGGTGAGGGGAGGTCGAAGTGTCTCCACGCA	1921	2942	AGCTGTCCGGCTCCGACTCAATGCTGTAGCATATTACCGGGCTTGTATGATCGTCA	3001
Db	2511	GCTCAGCGCGGACAGAACAGGTGAGGGGAGGTCGAAGTGTCTCCACGCA	2570	3591	AGCTGTCCGGCTCCGACTCAATGCTGTAGCATATTACCGGGCTTGTATGATCGTCA	3650
Qy	1922	CACATCTTCTGCGGACTGCTGCTCAATGGGCTGTGTTGGACTGTCTATCATGTTGCGG	1981	3002	TACCAACTAGCGGAGACGCTCATTTGTGTAGCAACCGAGCGCTTAATGACGGGCTTTACCG	3061
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Qy	1982	GCTCAAGACCTTTGCGGCCCCAAAGGGCCATACCCAAATGTACCAATGTGGAC	2041	3062	GGGATTTCCAGTGTGATGCTGCAATACATGTGTACCCAGACAGTCTGAGCTTCAGGC	3121
Db	2631	GCTCAAGACCTTTGCGGCCCCAAAGGGCCATACCCAAATGTACCAATGTGGAC	2690	3711	GGGATTTCCAGTGTGATGCTGCAATACATGTGTACCCAGACAGTCTGAGCTTCAGGC	3770
Qy	2042	AGGACCTGCTGCTGACAGCGCCCCCGGGCGGCTTCTTTGACACCATGACCTGCG	2101	3122	TGAGCCCGACCTTACCATTTGAGACCGGACCGCTGCGCACCAAGACCGGCTGACGCTCGC	3830
Db	2691	AGGACCTGCTGCTGACAGCGCCCCCGGGCGGCTTCTTTGACACCATGACCTGCG	2750	3771	TGAGCCCGACCTTACCATTTGAGACCGGACCGCTGCGCACCAAGACCGGCTGACGCTCGC	3890
Qy	2102	GCAGCTCGGACCTTTACTTGGTCAAGGAGCATGCCGATGTCATTCGGGTGCGCGCGGG	2161	3182	AGCGGCGAGGACGAGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGAG	3241
				3831	AGCGGCGAGGACGAGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGAG	3890

3242 AACGGCCCTCGGCGATGTTTCGATTCCTCGGTTCTGCGAGTGTATGACGCGGGCTGTG 3301
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3951 CTTGGTACGAGCTCAGCGCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACAC 4010
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DB |||||
QY 8631 GATCAAGT 8638
DB |||||

RESULT 12

US-10-029-907-2
; Sequence 2, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: HEPATITIS C VIRUS
; CURRENT APPLICATION NUMBER: 13/083
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 2001-12-21
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8642
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
; NAME/KEY: variation
; LOCATION: 6268
; OTHER INFORMATION: r = a or g
; NAME/KEY: variation
; LOCATION: 4446
; OTHER INFORMATION: r = a or g
US-10-029-907-2

Query Match 90.7%; Score 7246.8; DB 4; Length 8642;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 7966; Conservative 2; Mismatches 9; Indels 675; Gaps 4;
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1202	AGACCAACACGGTTTCCTCTAGCGGATCAATTCG-----CCCCCCCCCTA	1250	1804	-----	1803
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1251	ACGTTACTGGCCGAAGCCGCTTGGAAATAAGCCGGTGTGCGTTGTCTATATGTTATTTT	1310	Db		1803
1310	CCACCATATTCGCGTCTTTTGGCAATGTAGGCCCCGGAACCTGGCCCTGCTCTCTTGA	1369	Qy		
1311	CCACCATATTCGCGTCTTTTGGCAATGTAGGCCCCGGAACCTGGCCCTGCTCTCTTGA	1370	Db		
1370	CGAGCATTCCTAGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGGAATGTGCG	1429	Qy		
1371	CGAGCATTCCTAGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGGAATGTGCG	1430	Db		
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1610	AAAGAGTCAAAATGGCTCTCCTCAAGGCTATTCAACAAGGGCTGAAGGATGCCAGAAG	1669	Qy		
1611	AAAGAGTCAAAATGGCTCTCCTCAAGGCTATTCAACAAGGGCTGAAGGATGCCAGAAG	1670	Db		
1670	TACCCCATTTGATGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTAGT	1729	Qy		
1671	TACCCCATTTGATGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTTAGT	1730	Db		
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1731	CGAGTTTAAAGAGCTAGGCCCCCGAACCAACCGGACGTGTTTCTTTGAAAAAC	1790	Db		
1790	ACGATAATACCATG-----	1803	Qy		
1791	ACGATAATACCATGACCGGAGATGCGCATCGTGGAGGCGCGTTTTCGTAGGTC	1850	Db		
1804	-----	1803	Qy		
1851	TGATACTTTGACCTTTGTACCGCACTATAAGTGTTCCTCGTAGGCTCATATGTTGTT	1910	Db		
1804	-----	1803	Qy		
1911	TACAATATTTTATCACAGGCGGAGGACACTTGCAGTGTGGATCCCCCCTCAACG	1970	Db		
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1804	-----	1803	Qy		
2091	TAAACCAAGTCCGTACTTCTGTCGGGACACAGGGCTCATTCGTGCATGCATGCTGTGC	2150	Db		
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2151	GGAGGTTGCTGGGGTCAATTATGTCCAAATGGCTCTCATGAAGTTGGCGCATGACAG	2210	Db		
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2211	GTACGTACGTTTATGACCATCTCACCCACTGCGGACTGGGCCACGCGGGCTACGAG	2270	Db		
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2271	ACCTTGGGTGGAGTTGAGCCCGTCTCTCTGTATGATGAGACCAAGGTTATCACCT	2330	Db		
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2391	GGGGGAGGAGATCATCTGGGACCGGACAGCCCTTGAAGGGCAGGGTGGGACTCC	2450	Db		
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2451	TCGCGCTTATTACGGCTTACTCCCAACAGACGCGAGGCTTCTTGGCTGCATCATCACTA	2510	Db		
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1862	GCCTCAGAGCGCGGACAGGAACCAAGTCTGAGGGGAGGTCCAAAGTGTCTCCACCGCAA	1921	Qy		
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Db	5631	CTGCTGAGGAGTACCTGAGGTTTACCGCGGTGGGGATTTTCCACTACGTGACGGGATGA	5690
Qy	5042	CCACTGACAAAGTAAAGTGGCCGTGTGAGGTTCCGGGCCCCCAAAATTTCTTCAGAAAGTGG	5101
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Qy	5102	ATGGGGTGGGGTGCACAGGTAGCTCCAGCGTGAACCCCTCTTACCGGGAGGAGTCA	5161
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Qy	5162	CATTCTGCTGGGGTCAATCAATACCTGTTGGGTCAAGCTCCCATCGGAGCCCCGAAC	5221
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Qy	5402	TCATCGAGGCAACCTCTGTGGCGGAGGAGTGGGGGAAATCAACCCGCTGGAGT	5461
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Qy	5522	GGGAGTATCCGTTCCCGCGGAGATCTTCGCGAGGTCCAGGAATTCCTCGAGGATGC	5581
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Qy	5582	CCATATGGGACGCGCGATTAACACCTCCACTGTAGTCTCTGAGGAGGACCGGACT	5641
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Qy	5642	AGTCCCTCCAGTGTGACGCGGTGTCATTCGCGGCTGCCAAGGCCCCCTCCGATCCAC	5701
Db	6291	AGTCCCTCCAGTGTGACGCGGTGTCATTCGCGGCTGCCAAGGCCCCCTCCGATCCAC	6350
Qy	5702	CTCCACGGAGGAGGACGGTGTCTGTCAAGTCTACCGTGTCTTCTGCTTGGCGG	5761
Db	6351	CTCCACGGAGGAGGACGGTGTCTGTCAAGTCTACCGTGTCTTCTGCTTGGCGG	6410
Qy	5762	AGTCCGCAAAAGACTTTGGGAGCTCCGAGTCTGTCGCGCGTCCGACGCGCACGGCAA	5821
Db	6411	AGTCCGCAAAAGACTTTGGGAGCTCCGAGTCTGTCGCGCGTCCGACGCGCACGGCAA	6470
Qy	5822	CGGCTCTCTGACACGAGCCCTCCGACGACGGCGACCGGGATCCGAGTGTGAGTGTACT	5881
Db	6471	CGGCTCTCTGACACGAGCCCTCCGACGACGGCGACCGGGATCCGAGTGTGAGTGTACT	6530
Qy	5882	CCTCCATGCCCCCTTGGGGGAGCGCGGGGATCCGATCTCAGCGAGGGGTCTTGGT	5941
Db	6531	CCTCCATGCCCCCTTGGGGGAGCGCGGGGATCCGATCTCAGCGAGGGGTCTTGGT	6590
Qy	5942	CTACCGTAAGCGAGGAGTGTAGGAGCTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGT	6001
Db	6591	CTACCGTAAGCGAGGAGTGTAGGAGCTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGT	6650
Qy	6002	CAGCGCCCTGATCAGCGCATGCGCTCGGAGGAAACCAAGCTGCCCATCATGCTGATGA	6061
Db	6651	CAGCGCCCTGATCAGCGCATGCGCTCGGAGGAAACCAAGCTGCCCATCATGCTGATGA	6710
Qy	6062	GCAACTCTTTGCTCGTCCACCAAACTTTGGTCTATGTCTACAACTCTCGCAGCGCAAGCC	6121
Db	6711	GCAACTCTTTGCTCGTCCACCAAACTTTGGTCTATGTCTACAACTCTCGCAGCGCAAGCC	6770
Qy	6122	TGCGGCAGAAAGTACCTTTTGACAGACTTCAGAGTCTCTGACGACCACTACCGGAGCG	6181
Db	6771	TGCGGCAGAAAGTACCTTTTGACAGACTTCAGAGTCTCTGACGACCACTACCGGAGCG	6830
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Qy	6242	AAGCCTGTAAAGTACGCCCCCACCATTTCGCGCAGATCTAAATTTGGCTATGGGGCAAGG	6301
Db	6891	AAGCCTGTAAAGTACGCCCCCACCATTTCGCGCAGATCTAAATTTGGCTATGGGGCAAGG	6950
Qy	6302	ACGTCCGGAACTTATCCAGCAAGCGGTTAAACACATCCGCTCCGTGTGGAAAGACTTGC	6361
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Qy	6482	TTCCGTGTGTCGAGAAATGGCCCTTTACGATGTGTCTCCACCTCCCTCAGGCCGTGA	6541
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Qy	6542	TGGGCTCTTTCATACGATTTCCATATCTCTCTGACAGCGGCTCGATTCCTGTTGAATG	6601
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Qy	6722	CCGAAAGCAGACAGGCCATTAAGTCTGCTCACAGCGGCTTTACATCGGGGCCCCCTGA	6781
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Db	7431	CTAATTTCTAAGGGCAGAACTCGGCTATCGCGGTGCGCGCGAGCGGTGTACTGACGA	7490
Qy	6842	CCAGCTGCGGTAAATACCTTCACATGTTACTTGAAGCGCGCTCGGCTCTCGAGCTGCGA	6901
Db	7491	CCAGCTGCGGTAAATACCTTCACATGTTACTTGAAGCGCGCTCGGCTCTCGAGCTGCGA	7550
Qy	6902	AGCTCCAGAGTGCAGATGCTGCTGATGCGGAGACGACCTTCGTTATCTGTGAAAGCG	6961
Db	7551	AGCTCCAGAGTGCAGATGCTGCTGATGCGGAGACGACCTTCGTTATCTGTGAAAGCG	7610
Qy	6962	CGGGGACCCAGAGGACGAGCGGCTTACGGGCTTTCAGGAGGCTATGACTAGTACT	7021
Db	7611	CGGGGACCCAGAGGACGAGCGGCTTACGGGCTTTCAGGAGGCTATGACTAGTACT	7670
Qy	7022	CTCCCCCTCTGGGGACCCGCCCAAAACCAAGATTAAGCTTTGAGTGTGATCAATCATGCT	7081
Db	7671	CTCCCCCTCTGGGGACCCGCCCAAAACCAAGATTAAGCTTTGAGTGTGATCAATCATGCT	7730
Qy	7082	CTTCCAAATGTGATGCTGCGCAGATGCTATCGGAAAGGGTGTACTATCTCACCCGCTG	7141
Db	7731	CTTCCAAATGTGATGCTGCGCAGATGCTATCGGAAAGGGTGTACTATCTCACCCGCTG	7790

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Db 7791 ACCCACACCCCTTTCGGGGCTGGTGGGAGACAGCTAGACACACTCCAGTCAATT 7850
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RESULT 13

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US-10-029-907-6
; Sequence 6, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
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; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)... (8407)
; US-10-029-907-6
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Query Match 90.7%; Score 7245.6; DB 4; Length 8638;
Best Local Similarity 92.0%; Pred. No. 0;
Matches 7958; Conservative 0; Mismatches 19; Indels 671; Gaps 3;

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QY 842 TGTGATCAGATGATCTGGAGCAAGAGCATAGGGGCTCGGGGCTCGGCGGCAAGTCTTCCG 901
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842	TGTCGATCAGGATGATCTGGACGAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCCG	901	1911	TACAATATTTTATCACAGGCGGAGGCACACATTTGCAAGTGTGGATCCCCCCCCCTCAACG	1970
902	CAGGCTCAAGGCGCGCATGCCGCGGAGGATCTCGTGTGACCCATGCGGATGCGCTG	961	1804	-----	1803
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962	CTTGCCGAATATCATGCTGGAAATGGCGCTTTCTCGAATCATCGACTGTGGCGGCT	1021	1804	-----	1803
962	CTTGCCGAATATCATGCTGGAAATGGCGCTTTCTCGAATCATCGACTGTGGCGGCT	1021	2031	TTACCATCACAAATCTTGTGCGCATACTCGGTCCACTCATGTGTCTCCAGGCTGGTA	2090
1022	GGGTGTGGCGGACCGCTATCAGACATAGCGTGGCTACCCGTGATTTGCTGAAGAGCT	1081	1804	-----	1803
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1082	TGGCGGGAATGGCTGACCGCTTCTCTGCTTTACGCTATCGCGCTCCCGATTCGCA	1141	1804	-----	1803
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1142	GCGCATCGCTTCTATCGCTTCTTCAACGAGTTCTTCTGAGTT-----TAAAC	1189	1804	-----	1803
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1250	ACGTTACTGCGGAGCGCTTGGAAATAGGCGCGGTGCTGCTGCTATATGTTATTTT	1309	1804	-----	1803
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1310	CCACCATATTTGCCGTTTGGCAATGTAGGGCCCGGAACCTGGCCCTGCTCTTTGA	1369	1804	-----	1803
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1370	CGAGCATCTTAGGGGTTTCCCTCTCGCAAGGAATGCAAGGCTGTGTTGAATGTCG	1429	1804	--GCGCCTATTAGGCGCTACTCCCAACAGACGCGAGGCTACTTTGGTGTGATCATCTA	1861
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1430	TGAAGGAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACACGCTGTGAGGACCCCTT	1489	1862	GCCTCACAGGCGGGAAGGAAACAGGTCCGAGGGGAGGTCCAAAGTGTCTCCACCGCAA	1921
1431	TGAAGGAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACACGCTGTGAGGACCCCTT	1490	2511	GCCTCACAGGCGGGAAGGAAACAGGTTCGAGGGGAGGTCCAAAGTGTCTCCACCGCAA	2570
1490	CGAGCAGCGGAACCCCGACCTGCGGACAGGTGCTCTGGGCGCAAGGCTGAT	1549	1922	CACATCTTTCTCGGCGACTGCGTCAATGCGGTGTGTGACTGTCTATCATGTGCGG	1981
1491	CGAGCAGCGGAACCCCGACCTGCGGACAGGTGCTCTGGGCGCAAGGCTGAT	1550	2571	CACATCTTTCTCGGCGACTGCGTCAATGCGGTGTGTGACTGTCTATCATGTGCGG	2630
1550	AAGATACACCTGCAAGGCGGCACAAACCCAGTGCACGTTGTGAGTTGGATGTTGG	1609	1982	GCTCAAGACACCTTGGCGGCCCAAGGCGCCCAATCACCAGGCTGTACCAATGTGGACC	2041
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1610	AAAGAGTCAATGGCTCTCTCAAGGCTATTCACAAAGGGGCTGAAGATGCCAGAGG	1669	2042	AGGACCTCGTGGGTGGCAAGCGGCCCGGGGCGGTTCCTTGACACCATGCACTGCG	2101
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1670	TACCCCATGTATGGATCTGATCTGGGCGCTCGGTGACATGCTTTACATGTTAGT	1729	2102	GCAGTCTCGGACCTTTACTTTGTCACGAGCATGCGGATGTCAATCCGGTGCAGCGGCGG	2161
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1730	CGAGGTTAAACAGTCTAGGCCCCCGAAACACAGGGGACGTGGTTTCTTTGAAAAAC	1789	2162	GGCAGACAGAGGGGAGGCTTACTCTCCCGGCGGTCTCTCTACTTTGAAGGCTCTTCG	2221
1731	CGAGGTTAAACAGTCTAGGCCCCCGAAACACAGGGGACGTGGTTTCTTTGAAAAAC	1790	2811	GGCAGCGGACAGGGGAGGCTTACTCTCCCGGCGGTCTCTCTACTTTGAAGGCTCTTCG	2870
1790	ACGATAATACCATG-----	1803	2222	GGGCTCCATGCTCTGCTCCCTCGGCGACGCTGTGGCATCTTTCCGGGTGCCGCTGCA	2281
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1804	-----	1803	2282	CCGAGGGGTTGGAAGGGGCTGGAATTTGTACCCCTCGAGTCTATGGAACCATATGC	2341
1851	TGATACTCTTGACCTTGACCGCACTAATAGCTGTCTCGTAGGCTCATATGGTGGT	1910	2931	CCGAGGGGTTGGAAGGGGCTGGAATTTGTACCCCTCGAGTCTATGGAACCATATGC	2990
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			2991	GGTCCCCGGTCTTCAAGGCAACTCGTCCCTCGGCGGCTACCGAGACATTCAGGTGG	3050

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Db	3111	CCCAAGGGTATAAGGTGCTTGTCTCTGAA	CCCGTCCGTGCGCGCACCTAGGTTTCGGGG	3170
QY	2522	CGTATATGTCTAAGGCACATGTTATCGACCCCTAA	CATCAGAACCGGGGTAAAGCACATCA	2581
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QY	2582	CCACGGGTGCCCCCTACAGTACTCCACCTATG	GCAGAGTTTCTTTCGCGAGGTGTTGCT	2641
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QY	2642	CTGGGGGGCGCTATGACATCATTAATATGTGATG	AGTGCACCTCAACTGACTCGACCATTA	2701
Db	3291	CTGGGGGGCGCTATGACATCATTAATATGTGATG	AGTGCACCTCAACTGACTCGACCATTA	3350
QY	2702	TCCTTGGGCATCGGCACAGTCTCTGGACCAAG	CGGAGACCGCTCGAGGGCGACTCTGCTGTC	2761
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QY	2762	TCGCCACCGTACGCTCCGGGATCGGTACCGTGC	CAATCCAAACATCCGATCGAGAGGTGG	2821
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QY	3122	TGGACCCGACCTTACCAATTGAGACGACCG	TGCCAAGACGCGGTGTCAACGCTCGC	3181
Db	3771	TGGACCCGACCTTACCAATTGAGACGACCG	TGCCAAGACGCGGTGTCAACGCTCGC	3830
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Db	3831	AGCGCGAGGACGAGTCTGTAGGGGAGGATGG	GCATTTACAGTTTGTGACTCCAGGAG	3890
QY	3242	AACGGGCTTCGGGCATGTTTCGATTCTCTG	CGGAGTCTGTATGACGGGGCTGTG	3301
Db	3891	AACGGGCTTCGGGCATGTTTCGATTCTCTG	CGGAGTCTGTATGACGGGGCTGTG	3950
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Db	3951	CTTGTGTACGAGTCTACGCCCGCGAGAC	CTCAGTTAGGTTTGGGGCTTACCTAAACACAC	4010
QY	3362	CAGGGTTGCCCTCTGCCAGGACCATCTGG	AGTTCTGGGAGAGCGTCTTTACAGGCTCA	3421
Db	4011	CAGGGTTGCCCTCTGCCAGGACCATCTGG	AGTTCTGGGAGAGCGTCTTTACAGGCTCA	4070
QY	3422	CCCATAGACGCCCATTTCTTGTCCAGACTA	AGCAGGACGAGACAACTTCCCTTACC	3481
Db	4071	CCCATAGACGCCCATTTCTTGTCCAGACTA	AGCAGGACGAGACAACTTCCCTTACC	4130

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Db	4131	TGTTAGCATACCAAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGACC	4190
QY	3542	AAATGTGGAAGTGTTCTCATACGGCTAAAGCCTACGCTGCACGGGCCAAAGCCCTCGTGT	3601
Db	4191	AAATGTGGAAGTGTTCTCATACGGCTAAAGCCTAACGCTACGCTGCACGGGCCAAAGCCCTCGTGT	4250
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QY	3662	TGGCATATGATGTCGCTACCTTGSAGGTCTCACAGCACCTTGGGTGCTGTAGGCGGAG	3721
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QY	3782	TCATCTTCTCCGAAAAGCCGGSCATCTTCCGACAGGAGTCTCTTACCGGGATTCG	3841
Db	4431	TCATCTTCTCCGAAAAGCCGGSCATCTTCCGACAGGAGTCTCTTACCGGGATTCG	4490
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Db	4491	ATGAGATGGAAGATGGCCCTCACACCTCCCTTACATCGAAACAGGGAATGCAGCTCGCG	4550
QY	3902	AACAATTCACACAGAGGCATTCGGTTGCTGTGCAACAGCCACCAAGCAAGCGGAGGCTG	3961
Db	4551	AACAATTCACACAGAGGCATTCGGTTGCTGTGCAACAGCCACCAAGCAAGCGGAGGCTG	4610
QY	3962	CTGCTCCCGTGGTGGAAATCCAAGTGGCGACCCCTCGAAGCCCTCTGCGCGAGGACATATGT	4021
Db	4611	CTGCTCCCGTGGTGGAAATCCAAGTGGCGACCCCTCGAAGCCCTCTGCGCGAGGACATATGT	4080
QY	4022	GGAATTTTCATCAGCGGGATACAATATTAGAGGCTTTGTCCACTCTGCTGGCAACCCCG	4081
Db	4671	GGAATTTTCATCAGCGGGATACAATATTAGAGGCTTTGTCCACTCTGCTGGCAACCCCG	4730
QY	4082	CGATAGCATCACTGATGGCAATTCACAGCCCTTATCACAGCCCGCTCACCAACCAACATA	4141
Db	4731	CGATAGCATCACTGATGGCAATTCACAGCCCTTATCACAGCCCGCTCACCAACCAACATA	4790
QY	4142	CCCTCCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCCAACTTGCTCTCCACGCGCTG	4201
Db	4791	CCCTCCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCCAACTTGCTCTCCACGCGCTG	4850
QY	4202	CCTCTCCTTTCGTAGCGCGCGGATCGCTGGAGCGGCTGTGGCAGCATAGGCTTTGGGA	4261
Db	4851	CCTCTCCTTTCGTAGCGCGCGGATCGCTGGAGCGGCTGTGGCAGCATAGGCTTTGGGA	4910
QY	4262	AGGTGCTTGTGATATTTTGGCAGGTATTAGGACAGGGGTGGCAGCGCGCTGTGGCCT	4321
Db	4911	AGGTGCTTGTGATATTTTGGCAGGTATTAGGACAGGGGTGGCAGCGCGCTGTGGCCT	4970
QY	4322	TTAAGGTCTATGACGGCGAGATGCCCTCACCGAGGACCTGGTTAACTTACTTCCCTGCTA	4381
Db	4971	TTAAGGTCTATGACGGCGAGATGCCCTCACCGAGGACCTGGTTAACTTACTTCCCTGCTA	5030
QY	4382	TCCTCTCCCTTCGCGCCCTAGTTCGTGGGGTCTGTGGCAGGATPATGCGTCCGACG	4441
Db	5031	TCCTCTCCCTTCGCGCCCTAGTTCGTGGGGTCTGTGGCAGGATPATGCGTCCGACG	5090
QY	4442	TGGGCCACGGGAGGGGGCTGTGCAGTGTGAACCGGCTGTAGGTTGCTTCCGGG	4501
Db	5091	TGGGCCACGGGAGGGGGCTGTGCAGTGTGAACCGGCTGTAGGTTGCTTCCGGG	5150
QY	4502	GTAACCAAGTCTCCCCACGCACTATGTGTCCTGAGAGCGACGCTCAGCACGTGTGCACTC	4561
Db	5151	GTAACCAAGTCTCCCCACGCACTATGTGTCCTGAGAGCGACGCTCAGCACGTGTGCACTC	5210
QY	4562	AGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGGAAGGCTTCACCAAGTGAATCAACG	4621

5211	AGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAAGAGGCTTCCACGATGGATCAACG	5270	6291	ACGTCCCTCCAGTGGTACACGGGTGTCTCACTGCGCCCTGCCAAGGCGCCCTCCGATACCAC	6350
4622	AGGACTGTCTCACGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTGGATATGCA	4681	5702	CTCCACGAGGAAGAGGACGGTGTCTGTGTCAGAAATPACCGGTCTCTTCTGCTTGGCGG	5761
5271	AGGACTGTCTCACGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTGGATATGCA	5330	6351	CTCCACGAGGAAGAGGACGGTGTCTGTGTCAGAAATPACCGGTCTCTTCTGCTTGGCGG	6410
4682	CGGTGTGATGATTTCAAGACCTCGCTCCAGTCCAAAGCTCTGCGCGGATTTGCGGGAG	4741	5762	AGTCCGCCACAAAGACCTTTCGGCAGCTCCGAATCGTCCGCGGTTCGACAGCGGACCGGAA	5821
5331	CGGTGTGATGATTTCAAGACCTCGCTCCAGTCCAAAGCTCTGCGCGGATTTGCGGGAG	5390	6411	AGTCCGCCACAAAGACCTTTCGGCAGCTCCGAATCGTCCGCGGTTCGACAGCGGACCGGAA	6470
4742	TCCCTCTCTTCAATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	4801	5822	CGGCTCTCTTCAATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	5881
5391	TCCCTCTCTTCAATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	5450	6471	CGGCTCTCTTCAATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	6530
4802	AAACCACTGCGCCATGTGGAGACACATCAACCGGACATGTGAAACCGTTCATGAGGA	4861	5882	CTTCCATGCCCCCTTGAAGGGGAGCGCGGGGATCCCGATCTCAGCAGCGGCTTGGT	5941
5451	AAACCACTGCGCCATGTGGAGACACATCAACCGGACATGTGAAACCGTTCATGAGGA	5510	6531	CTTCCATGCCCCCTTGAAGGGGAGCGCGGGGATCCCGATCTCAGCAGCGGCTTGGT	6590
4862	TGCTGGGGCTTAGGACCTGTAGTAAACGCTGATGGAACATTTCCCGATTAACGCGTACA	4921	5942	CTACCGTAAAGGAGGAGGCTAGTAGGAGGCTGTGCTGCTCGATGTCTACACATGGA	6001
5511	TGCTGGGGCTTAGGACCTGTAGTAAACGCTGATGGAACATTTCCCGATTAACGCGTACA	5570	6591	CTACCGTAAAGGAGGAGGCTAGTAGGAGGCTGTGCTGCTCGATGTCTACACATGGA	6650
4922	CCAGGGCCCCCTGACGCCCTCCCGCGCCAAATTTCTAGGGGCTGTGGCGGTGG	4981	6002	CAGGCGCCCTGATCACGCCATCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTGA	6061
5571	CCAGGGCCCCCTGACGCCCTCCCGCGCCAAATTTCTAGGGGCTGTGGCGGTGG	5630	6651	CAGGCGCCCTGATCACGCCATCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTGA	6710
4982	CTGCTGAGGAGTACGTGGAGGTACGCGGGTGGGGATTTCCACTAGCTGACGGGCATGA	5041	6062	GCAACTCTTTGCTCCGCTCACCAACCTTGTGTATGTCTATGCTCAACATCTCGCAGCGCAGCC	6121
5631	CTGCTGAGGAGTACGTGGAGGTACGCGGGTGGGGATTTCCACTAGCTGACGGGCATGA	5690	6711	GCAACTCTTTGCTCCGCTCACCAACCTTGTGTATGTCTATGCTCAACATCTCGCAGCGCAGCC	6770
5042	CACTGACAAAGTAAAGTGGCCGTGTGAGTTCGGGCCCGGAAATTTCTTACAGAAATGG	5101	6122	TGCGGCAAGAAAGAGTCACTTTGACAGACTGCGAGGTCTCGGACGACCACTTACCGGACG	6181
5691	CACTGACAAAGTAAAGTGGCCGTGTGAGTTCGGGCCCGGAAATTTCTTACAGAAATGG	5750	6771	TGCGGCAAGAAAGAGTCACTTTGACAGACTGCGAGGTCTCGGACGACCACTTACCGGACG	6830
5102	ATGGGGTGGCTTGCACAGGTACGCTCCAGCTGCAACCTCTCTAGGGAGGAGTCA	5161	6182	TGCTCAAGGAGATGAAGCGGAAAGCGCTCCAGTGAAGGCTTAACTTCTATCCGTGAGG	6241
5751	ATGGGGTGGCTTGCACAGGTACGCTCCAGCTGCAACCTCTCTAGGGAGGAGTCA	5810	6831	TGCTCAAGGAGATGAAGCGGAAAGCGCTCCAGTGAAGGCTTAACTTCTATCCGTGAGG	6890
5162	CATTCTGGTGGGCTCAATCAATACCTGTTGGGTCAAGCTCCCATGCGAGCCGAAAC	5221	6242	AAGCTGTGTAAGCTGACGCCGCCCAANTCGGCCAGATCTAAATTTGGCTATCGGCGCAAGG	6301
5811	CATTCTGGTGGGCTCAATCAATACCTGTTGGGTCAAGCTCCCATGCGAGCCGAAAC	5870	6891	AAGCTGTGTAAGCTGACGCCGCCCAANTCGGCCAGATCTAAATTTGGCTATCGGCGCAAGG	6950
5222	CGGAGTACAGTGTCTATTCATGCTCAACGACCTTCCCACTTCCAGTCCAGTACGCTAGC	5281	6302	ACGTCCGGAACCTTATCCAGAAAGCGGTTAACACATCCGCTCCGTGTTGGAGGACTTGC	6361
5871	CGGAGTACAGTGTCTATTCATGCTCAACGACCTTCCCACTTCCAGTCCAGTACGCTAGC	5930	6951	ACGTCCGGAACCTTATCCAGAAAGCGGTTAACACATCCGCTCCGTGTTGGAGGACTTGC	7010
5282	CTAAGCGTAGGTGCGCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCCAGC	5341	6362	TGGAGACACTGAGACACCAATTCACACCACTCATGCGCAAAATAAATGAGGTTTCTGCG	6421
5931	CTAAGCGTAGGTGCGCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCCAGC	5990	7011	TGGAGACACTGAGACACCAATTCACACCACTCATGCGCAAAATAAATGAGGTTTCTGCG	7070
5342	TGCTCGGCTTCTTCTTGAAGCAACATGACCTTACCTTCCAGTCCCGGACGCTGACC	5401	6422	TCCAAACAGAGAGGGGGGCGCAAGCCAGCTGCGCTTATCGTATTCAGATTTGGGGG	6481
5991	TGCTCGGCTTCTTCTTGAAGCAACATGACCTTACCTTCCAGTCCCGGACGCTGACC	6050	7071	TCCAAACAGAGAGGGGGGCGCAAGCCAGCTGCGCTTATCGTATTCAGATTTGGGGG	7130
5402	TCATCGAGCCCACTCTCTGCGGCGAGGATGGCGGGGAACATCACCGCGTGGAGT	5461	6482	TTCTGTGTGCGAGAAATGGCCCTTTAGCATGTGCTTCCACCTTCCCTCAGGCGGTGA	6541
6051	TCATCGAGCCCACTCTCTGCGGCGAGGATGGCGGGGAACATCACCGCGTGGAGT	6110	7131	TTCTGTGTGCGAGAAATGGCCCTTTAGCATGTGCTTCCACCTTCCCTCAGGCGGTGA	7190
5462	CAGAAATAAGTGTATTTTGGACTTTTGGAGCTTTTGGAGCTTTTGGAGCTTTTGGAG	5521	6542	TGGGCTCTTCTATACCGATTTCCAAATCTCTCTTCCGAGCGGCTGAGGTTCTGCTGGAATG	6601
6111	CAGAAATAAGTGTATTTTGGACTTTTGGAGCTTTTGGAGCTTTTGGAGCTTTTGGAG	6170	7191	TGGGCTCTTCTATACCGATTTCCAAATCTCTCTTCCGAGCGGCTGAGGTTCTGCTGGAATG	7250
5522	GGGAGTATCCGTTCCGGGGGAGATCTCGGAGGTCCAGGAAATTCCTTCGAGCGATGC	5581	6602	CCTGGAAGCGAAGAAATGCCCTATAGGGCTTCGATATGACACCGCTGTTTGAATCAA	6661
6171	GGGAGTATCCGTTCCGGGGGAGATCTCGGAGGTCCAGGAAATTCCTTCGAGCGATGC	6230	7251	CCTGGAAGCGAAGAAATGCCCTATAGGGCTTCGATATGACACCGCTGTTTGAATCAA	7310
5582	CCATATGGGCAAGCGGATTAACAACTTCACTGTAGAGTCTCGGAGGACCGGACT	5641	6662	CGGTCTAGAGATGACATCCGCTTGGAGGTCAATCTACCAATTTGTGACTTGGCCCC	6721
6231	CCATATGGGCAAGCGGATTAACAACTTCACTGTAGAGTCTCGGAGGACCGGACT	6290	7311	CGGTCTAGAGATGACATCCGCTTGGAGGTCAATCTACCAATTTGTGACTTGGCCCC	7370
5642	ACGTCCCTCCAGTGGTACAGGGTGTCCATTGCGCGCTGCAAGGCGCTTCCGATACCAC	5701	6722	CCGAGCCGACAGAGGCGATTAAGGTCTCAGAGCGGCTTTTACATCGGGGGCCCCCTGA	6781
			7371	CCGAGCCGACAGAGGCGATTAAGGTCTCAGAGCGGCTTTTACATCGGGGGCCCCCTGA	7430

QY	481	CTGATGCGCGCTGTTCCGGCTGTACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG	540	Db	1550	TAAGATACACCTGCAAGGGCGGCAACCCAGTCCACGTTGTGATGTTGTTG	1609
Db	481	CTGATGCGCGCTGTTCCGGCTGTACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCG	540	QY	1609	GAAAGAGTCAATGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGATGCCAGAG	1668
QY	541	ACCTGTCCGGTCCCTGATGAACTGACGAGGAGCGCGGTATCGTGGCTGGCCA	600	Db	1610	GAAAGAGTCAATGCTCTCTCAAGCGTATTCAAAGGGGCTGAAGATGCCAGAG	1669
Db	541	ACCTGTCCGGTCCCTGATGAACTGACGAGGAGCGCGGTATCGTGGCTGGCCA	600	QY	1669	GTACCCCATTTGATGGGATCTGATCTGGGGCTCGTGGACATGTTTACATGTTTAT	1728
QY	601	CGACGGGCTTCTTTCGCGAGCTGTCTGCAAGTTGTCTCACTGAAGCGGAAAGGACTGC	660	Db	1670	GTACCCCATTTGATGGGATCTGATCTGGGGCTCGTGGACATGTTTACATGTTTAT	1729
Db	601	CGACGGGCTTCTTTCGCGAGCTGTCTGCAAGTTGTCTCACTGAAGCGGAAAGGACTGC	660	QY	1729	TCAGGTTTAAAGAAAGTCTAGGCCCCCGAAACACGGGACGTTTCTTTTGAATAA	1788
QY	661	TGCTATTGGCGGAAGTCCGCGGCGAGGATCTCTGTCTCATCTCACTTGTCTCCGCGA	720	Db	1730	TCAGGTTTAAAGAAAGTCTAGGCCCCCGAAACACGGGACGTTTCTTTTGAATAA	1789
Db	661	TGCTATTGGCGGAAGTCCGCGGCGAGGATCTCTGTCTCATCTCACTTGTCTCCGCGA	720	QY	1789	CACGATAATACCATG-----	1803
QY	721	AGTATCCATCATGGCTGATGCAATGGCGGCTGCATACGTTGATCCGGCTACCTGCC	780	Db	1790	CACGATAATACCATGACCGGGAGATGGCAGCATCTGTGGAGCGCGTTCGTAGGT	1849
Db	721	AGTATCCATCATGGCTGATGCAATGGCGGCTGCATACGTTGATCCGGCTACCTGCC	780	QY	1804	-----	1803
QY	781	CATTGACACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCGCGTC	840	Db	1850	CTGATACTCTTGACCTTTGTACCGCACTATAAGCTGTTCTCGTAGGCTCATATGTTG	1909
Db	781	CATTGACACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCGCGTC	840	QY	1804	-----	1803
QY	841	TTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGGCCAGCGCACTGTTCG	900	Db	1910	TTACAAATATTTTATACAGGGCGGAGGACACATTGCAAGTGTGATCCCCCCCCCTCAAC	1969
Db	841	TTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGGCCAGCGCACTGTTCG	900	QY	1804	-----	1803
QY	901	CCAGGCTCAAGCGCGCATGCCGACGCGGAGGATCTGCTGCACCATGCGGCATGCT	960	Db	1970	GTTCGGGGGGCGCGATGCGTCACTCTCTCACGTGCGCATCCACCCAGAGCTAATC	2029
Db	901	CCAGGCTCAAGCGCGCATGCCGACGCGGAGGATCTGCTGCACCATGCGGCATGCT	960	QY	1804	-----	1803
QY	961	GCTTGGCGGAATCATGTTGAAATGCGCTTTTCTGGAATCATGACATGTGGCGGC	1020	Db	2030	TTTACCATCACCAAAATCTTGTCTCGCATACTCGTCCACTCATGTTGCTCCAGGCTGCT	2089
Db	961	GCTTGGCGGAATCATGTTGAAATGCGCTTTTCTGGAATCATGACATGTGGCGGC	1020	QY	1804	-----	1803
QY	1021	TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTCAATTTCTGAAGAGC	1080	Db	2090	ATAACCAAGTGCCTACTTCTGCGGCGCACACGGGCTCATTCGTGCATGCATGCTGTG	2149
Db	1021	TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTCAATTTCTGAAGAGC	1080	QY	1804	-----	1803
QY	1081	TTGGCGGGAATGGGCTGACCGTCTTCTGCTTTTACGGTATCGCCGCTCCCGATTCGC	1140	Db	2150	CGGAAGTTGCTGGGGTCAATTAATGTCCTCAATGCTCTCATGAAGTTGGCGGCTACGAC	2209
Db	1081	TTGGCGGGAATGGGCTGACCGTCTTCTGCTTTTACGGTATCGCCGCTCCCGATTCGC	1140	QY	1804	-----	1803
QY	1141	AGCGCATGCGCTTCTATCGCTTTCTGACAGTTCTCTGAGTT-----TAAA	1188	Db	2210	GGTACGTAGCTTTATGACCATCTCACCCACTGCGGGACTGGGCGCACCGGGCCCTACGA	2269
Db	1141	AGCGCATGCGCTTCTATCGCTTTCTGACAGTTCTCTGAGTT-----TAAA	1200	QY	1804	-----	1803
QY	1189	CAGACCAACACGTTTCCCTTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCT	1248	Db	2270	GACCTTGGGGTGGAGTTCGCTCTCTCTGATGAGACATCATCTTGGGCTGCGGCTTATCACC	2329
Db	1189	CAGACCAACACGTTTCCCTTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCT	1248	QY	1804	-----	1803
QY	1249	AAGCTTACTGCGGAGCGCTTGGAAATAGGCGGCTGTGCGTTTGTCTATATGTTATTT	1308	Db	2330	TGGGGGCGACACCGCGCGTGTGGGACATCATCTTGGGCTGCGGCTGCGGCGCGC	2389
Db	1249	AAGCTTACTGCGGAGCGCTTGGAAATAGGCGGCTGTGCGTTTGTCTATATGTTATTT	1309	QY	1804	-----	1803
QY	1309	TCCACCATATTGCGGTCTTTTGGCAATGTAGGGCGCGGAAACCTGGCCCTGTCTCTTG	1368	Db	2390	AGGGGAGGAGATACATCTGGACCGGACAGCAGCTTTGAAGGGCAGGGTGGCGACTC	2449
Db	1309	TCCACCATATTGCGGTCTTTTGGCAATGTAGGGCGCGGAAACCTGGCCCTGTCTCTTG	1369	QY	1804	-----	1803
QY	1369	ACGAGCATTCCTAGGGGTCTTTCCCTCTCGCAAGAGGATGCAAGTCTGTTGAATGTC	1428	Db	2450	CTCGCGCTTATACGGCTTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCACT	2509
Db	1369	ACGAGCATTCCTAGGGGTCTTTCCCTCTCGCAAGAGGATGCAAGTCTGTTGAATGTC	1429	QY	1861	AGCCTCACAGGCGGACAGGAACAGGTCGAGGGGAGTCCAAAGTGTCTCCACCGCA	1920
QY	1429	GTGAGGAAGCAGTCTCTGGAAGCTTCTTGAAGACAAACAGCTCTGAGGACCCCTT	1488	Db	2510	AGCCTCACAGGCGGACAGGAACAGGTCGAGGGGAGTCCAAAGTGTCTCCACCGCA	2569
Db	1429	GTGAGGAAGCAGTCTCTGGAAGCTTCTTGAAGACAAACAGCTCTGAGGACCCCTT	1489	QY	1921	ACAAATCTTTCTGGGCTCGTCAATGGCGTGTGTTGGACTGTCTATCATGTGTC	1980
QY	1489	TGACGAGCGGAAACCCCGACCTGCGGACAGGTGCTCTGCGCGCAAAAGCCACGTGA	1548	Db	2570	ACAAATCTTTCTGGGCTCGTCAATGGCGTGTGTTGGACTGTCTATCATGTGTC	2629
Db	1489	TGACGAGCGGAAACCCCGACCTGCGGACAGGTGCTCTGCGCGCAAAAGCCACGTGA	1549	QY	1981	GGCTCAAGACCTTTCGCGGCGGCAACCCAGGCGGCAATCAACCAATGTACCAATGTGAC	2040
QY	1549	TAAGATACACCTGCAAGGGCGCACACCCAGTGCACGTTGTGAGTTGGATGTTGTG	1608				

Db	2630	GGCTCAAGACCCCTTGC	CGGCCCAAGGGCCCAATC	ACCCAAATGTACACCAATGTGGAC	2689	
Qy	2041	CAGGACCTCGTCGGT	TGCAAGCGCCCCCGGGCGGGTTC	CTTTGACACCAATGACACCTGC	2100	
Db	2690	CAGGACCTCGTCGGT	TGCAAGCGCCCCCGGGCGGGTTC	CTTTGACACCAATGACACCTGC	2749	
Qy	2101	GGCAGCTCGGACCTT	TACTTGGTACAGAGGATCGGATGTCA	TCCTCGGTCGCGCGCGG	2160	
Db	2750	GGCAGCTCGGACCTT	TACTTGGTACAGAGGATCGGATGTCA	TCCTCGGTCGCGCGCGG	2809	
Qy	2161	GGCGACAGCGGGAGC	CTACTCTCCCGCAGAGCGGCTCTCTCT	TGAAAGGGCTCTTCG	2220	
Db	2810	GGCGACAGCGGGAGC	CTACTCTCCCGCAGAGCGGCTCTCTCT	TGAAAGGGCTCTTCG	2869	
Qy	2221	GGCGCTCCACTGCT	CTGCGCCCTCGGGGACCGCTGTGGGCA	TCCTTTCCGGGTCGCGTGTGC	2280	
Db	2870	GGCGCTCCACTGCT	CTGCGCCCTCGGGGACCGCTGTGGGCA	TCCTTTCCGGGTCGCGTGTGC	2929	
Qy	2281	ACCGAGGGGTTCG	GAAGGGGTGGACTTTGTACCCGTCAGTCT	ATATGGAAACCACTATG	2340	
Db	2930	ACCGAGGGGTTCG	GAAGGGGTGGACTTTGTACCCGTCAGTCT	ATATGGAAACCACTATG	2989	
Qy	2341	CGGTCCCGGTCTT	CAACGCAACTCGTCCCGCTCCGCGCGTAC	CGCAGACATTTCCAGGTG	2400	
Db	2990	CGGTCCCGGTCTT	CAACGCAACTCGTCCCGCTCCGCGCGTAC	CGCAGACATTTCCAGGTG	3049	
Qy	2401	GCCCATCTACG	CCCTTACTGTAGGGCAAGACACTAAGGTG	CGCGTGGTATGCA	2460	
Db	3050	GCCCATCTACG	CCCTTACTGTAGGGCAAGACACTAAGGTG	CGCGTGGTATGCA	3109	
Qy	2461	GCCCAAGGGTATA	AGGTGCTGTGCTGAACCCGTCGTCGCGCG	CAACCTAGTTCGGG	2520	
Db	3110	GCCCAAGGGTATA	AGGTGCTGTGCTGAACCCGTCGTCGCGCG	CAACCTAGTTCGGG	3169	
Qy	2521	GGGTATATGCTA	AGGCAATGATCGATCGACCCCTAA	CATCAGAACCGGGTAAGGACCATC	2580	
Db	3170	GGGTATATGCTA	AGGCAATGATCGATCGACCCCTAA	CATCAGAACCGGGTAAGGACCATC	3229	
Qy	2581	ACCAGGGTCCCG	CCATCAGTACTCCACCTATGGCAAGT	TTCTTCCGACCGGTGTGC	2640	
Db	3230	ACCAGGGTCCCG	CCATCAGTACTCCACCTATGGCAAGT	TTCTTCCGACCGGTGTGC	3289	
Qy	2641	TCTGGGGCGCCT	ATAGCATATATATGTATGATGGCCAT	CTAACTGACTCGACCACT	2700	
Db	3290	TCTGGGGCGCCT	ATAGCATATATATGTATGATGGCCAT	CTAACTGACTCGACCACT	3349	
Qy	2701	ATCTTGGGCAT	CGGCACAGTCTCGACCAAGCGGAGAC	CGGCTGGAGCGGACTCGTGTG	2760	
Db	3350	ATCTTGGGCAT	CGGCACAGTCTCGACCAAGCGGAGAC	CGGCTGGAGCGGACTCGTGTG	3409	
Qy	2761	CTCGCCACCGCT	ACGCTCGGGATCGGTACCGGTG	CCACATCCAAACATCGAGGAGTG	2820	
Db	3410	CTCGCCACCGCT	ACGCTCGGGATCGGTACCGGTG	CCACATCCAAACATCGAGGAGTG	3469	
Qy	2821	GCTGTCCAGCAT	CTGGAGAAATCCCTTTTATGGCAAGC	CAATCCCATCGAGACCATC	2880	
Db	3470	GCTGTCCAGCAT	CTGGAGAAATCCCTTTTATGGCAAGC	CAATCCCATCGAGACCATC	3529	
Qy	2881	AAGGGGGAGGCA	CCCTCATTTCTGCCATTCGAAGAAAT	GTGATGAGTACGTCGCGG	2940	
Db	3530	AAGGGGGAGGCA	CCCTCATTTCTGCCATTCGAAGAAAT	GTGATGAGTACGTCGCGG	3589	
Qy	2941	AAGCTGTCGG	CCCTCGGACTCAATGTGTAGCA	TATTTACCGGGCTTTGATGATCCGTC	3000	
Db	3590	AAGCTGTCGG	CCCTCGGACTCAATGTGTAGCA	TATTTACCGGGCTTTGATGATCCGTC	3649	
Qy	3001	ATACCAACTAG	CGAGACGTATGTCAGACGACGCT	CTATATGA	CGGGCTTTACC	3060
Db	3650	ATACCAACTAG	CGAGACGTATGTCAGACGACGCT	CTATATGA	CGGGCTTTACC	3709
Qy	3061	GGCGATTCG	ACTCAGTATCGACTGCAATATACAT	GTGTACCCAGACAGTTCGACTTCAGC	3120	
Db	3710	GGCGATTCG	ACTCAGTATCGACTGCAATATACAT	GTGTACCCAGACAGTTCGACTTCAGC	3769	
Qy	3121	CTGACCCGAC	CTTTCA	CAATGTAGACGACGACCGGTGTCA	CGCTCG	3180
Db	3770	CTGACCCGAC	CTTTCA	CAATGTAGACGACGACCGGTGTCA	CGCTCG	3829
Qy	3181	CAGCGGAGG	CAGGACTGTGTAGGGG	CAGGATGGGCAATTTACAGTTTGT	GACTCCAGGA	3240
Db	3830	CAGCGGAGG	CAGGACTGTGTAGGGG	CAGGATGGGCAATTTACAGTTTGT	GACTCCAGGA	3889
Qy	3241	GAACGGCCCT	CGGGCATGTTTCGATTCTCTCGG	TCTCTGTGCGAGTGTCTATGAC	CGCGGGTGT	3300
Db	3890	GAACGGCCCT	CGGGCATGTTTCGATTCTCTCGG	TCTCTGTGCGAGTGTCTATGAC	CGCGGGTGT	3949
Qy	3301	GCTTGTGTAC	GAGCTACGCGCCGCGAGACCT	CAGTTAGTTTGGGGCTTACCTAAACACA	3360	
Db	3950	GCTTGTGTAC	GAGCTACGCGCCGCGAGACCT	CAGTTAGTTTGGGGCTTACCTAAACACA	4009	
Qy	3361	CCAGGGTTG	CCCTCTGCGCAGGACCATCTGGAGT	TTCTGGAGAGCGTCTTTACAGGCCTC	3420	
Db	4010	CCAGGGTTG	CCCTCTGCGCAGGACCATCTGGAGT	TTCTGGAGAGCGTCTTTACAGGCCTC	4069	
Qy	3421	ACCCATAGAC	CCCAATTTCTTGTCCAGACTAAGC	CAGCAGGAGACACTTCCCTTAC	3480	
Db	4070	ACCCATAGAC	CCCAATTTCTTGTCCAGACTAAGC	CAGCAGGAGACACTTCCCTTAC	4129	
Qy	3481	CTGGTAGCAT	ATACAGGCTACGCTGTGCGCAGGGCT	CAGGCTCCACCTCATCTGCGGAC	3540	
Db	4130	CTGGTAGCAT	ATACAGGCTACGCTGTGCGCAGGGCT	CAGGCTCCACCTCATCTGCGGAC	4189	
Qy	3541	CAAAATGTGA	AGTGTCTCATACGGCTTAAGCC	TAGCTGCA	CGGGCAACGCCCTGTG	3600
Db	4190	CAAAATGTGA	AGTGTGTCTCATACGGCTTAAGCC	TAGCTGCA	CGGGCAACGCCCTGTG	4249
Qy	3601	TATAGCTTGG	AGCCGCTTCAAAACAGAGTTACT	TACACACACCCCATACCAAAATACATC	3660	
Db	4250	TATAGCTTGG	AGCCGCTTCAAAACAGAGTTACT	TACACACACCCCATACCAAAATACATC	4309	
Qy	3661	ATGGCATGAT	GTGCGCTGACCTGAGGTGTG	CAGGACACCTGCTGTGTAGGCGGA	3720	
Db	4310	ATGGCATGAT	GTGCGCTGACCTGAGGTGTG	CAGGACACCTGCTGTGTAGGCGGA	4369	
Qy	3721	GTCTTAGCAG	CTCGCGCGCTTATTCCTTGAC	CAACAGGAGCGTGTGCTTGTGGGCGG	3780	
Db	4370	GTCTTAGCAG	CTCGCGCGCTTATTCCTTGAC	CAACAGGAGCGTGTGCTTGTGGGCGG	4429	
Qy	3781	ATCATCTTGT	CCGGAAGCCGCGCATCATTTCCG	ACAGGAGTCTTACCGGAGTTC	3840	
Db	4430	ATCATCTTGT	CCGGAAGCCGCGCATCATTTCCG	ACAGGAGTCTTACCGGAGTTC	4489	
Qy	3841	GATGAGATGG	AGAGTGTGCTCTCACCTCCCTT	TACATCGAACAGGGAATG	CAGCTCGCC	3900
Db	4490	GATGAGATGG	AGAGTGTGCTCTCACCTCCCTT	TACATCGAACAGGGAATG	CAGCTCGCC	4549
Qy	3901	GAACAAATTC	CAACAGAGGCAATCGGTTGCTG	CAAAACAGCAACAGCGGAGGCT	3960	
Db	4550	GAACAAATTC	CAACAGAGGCAATCGGTTGCTG	CAAAACAGCAACAGCGGAGGCT	4609	
Qy	3961	GCTGCTCC	CGTGTGGAATCCAAAGTGTGCG	ACCTCTCGAAGCTTCTGCGGAGACATATG	4020	
Db	4610	GCTGCTCC	CGTGTGGAATCCAAAGTGTGCG	ACCTCTCGAAGCTTCTGCGGAGACATATG	4669	
Qy	4021	TGGAATTTCA	TACAGGGAATACAAATTTTAG	CAGGCTTGTCCACTCTGCTGGCAACCCC	4080	
Db	4670	TGGAATTTCA	TACAGGGAATACAAATTTTAG	CAGGCTTGTCCACTCTGCTGGCAACCCC	4729	
Qy	4081	GCATAGCAT	CTGATGCAATTCAGGCTCTAT	CAACAGCGGCTCACCACCCACAT	4140	
Db	4730	GCATAGCAT	CTGATGCAATTCAGGCTCTAT	CAACAGCGGCTCACCACCCACAT	4789	
Qy	4141	ACCTCTCT	GTGTTAAACATCTCGGGGGAT	GGGTGGCGCCCACTTCTCTCCAGGCT	4200	
Db	4790	ACCTCTCT	GTGTTAAACATCTCGGGGGAT	GGGTGGCGCCCACTTCTCTCCAGGCT	4849	

Db 7010 CTGGAAGACACTGAGACACCAATTGACACCACCATCATGGCAAAATAGAGTTTCTGC 7069
QY 6421 GTCCAAACAGAGAGGGGGCGGCAAGCCAGCTGCCTTATCGTATTCACAGATTGGGG 6480
Db 7070 GTCCAAACAGAGAGGGGGCGGCAAGCCAGCTGCCTTATCGTATTCACAGATTGGGG 7129
QY 6481 GTTCGTGTGTGCGAGAAATAGCCCTTTACAGATGTGTCTCCAGCTCCCTCAGGCCGTG 6540
Db 7130 GTTCGTGTGTGCGAGAAATAGCCCTTTACAGATGTGTCTCCAGCTCCCTCAGGCCGTG 7189
QY 6541 ATGGGCTCTTTCATACGGAATCCAAATCTCTCTCGACAGCGGTCGAGTTCCTGGTGAAT 6600
Db 7190 ATGGGCTCTTTCATACGGAATCCAAATCTCTCTCGACAGCGGTCGAGTTCCTGGTGAAT 7249
QY 6601 GCCTGGAACGAGAAATAGCCCTTTACAGATGTGTCTCCAGCTCCCTCAGGCCGTG 6660
Db 7250 GCCTGGAACGAGAAATAGCCCTTTACAGATGTGTCTCCAGCTCCCTCAGGCCGTG 7309
QY 6661 ACAGTCACTGAGAAATAGCCCTTTACAGATGTGTCTCCAGCTCCCTCAGGCCGTG 6720
Db 7310 ACAGTCACTGAGAAATAGCCCTTTACAGATGTGTCTCCAGCTCCCTCAGGCCGTG 7369
QY 6721 CCGGAAGCCAGACAGGCCATTAAGGTCTGCTCACAGAGCGGCTTTACATCGGGGGCCCTG 6780
Db 7370 CCGGAAGCCAGACAGGCCATTAAGGTCTGCTCACAGAGCGGCTTTACATCGGGGGCCCTG 7429
QY 6781 ACTAATTTCTAAGAGGAGAGATGCGGCTATCGCGGTATCGCGGTATCGCGGTATCGCGGT 6840
Db 7430 ACTAATTTCTAAGAGGAGAGATGCGGCTATCGCGGTATCGCGGTATCGCGGTATCGCGGT 7489
QY 6841 ACCAGTCCGAGTAAATACCTTCAATGCTGCTGAGAGCGGCTTTACATCGGGGGCCCTG 6900
Db 7490 ACCAGTCCGAGTAAATACCTTCAATGCTGCTGAGAGCGGCTTTACATCGGGGGCCCTG 7549
QY 6901 AAGTCTCAGGATGTCACGATGCTGCTGATCGGAGAGCGGCTTTACATCGGGGGCCCTG 6960
Db 7550 AAGTCTCAGGATGTCACGATGCTGCTGATCGGAGAGCGGCTTTACATCGGGGGCCCTG 7609
QY 6961 GCGGGAGCCCAAG 7020
Db 7610 GCGGGAGCCCAAG 7669
QY 7021 TCTGCCCCCTTGGGAGCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7080
Db 7670 TCTGCCCCCTTGGGAGCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7729
QY 7081 TCTTCAATGTGAGTCCGCGAG 7140
Db 7730 TCTTCAATGTGAGTCCGCGAG 7789
QY 7141 GACCCCAACCCCTTGGCGGGCTGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7200
Db 7790 GACCCCAACCCCTTGGCGGGCTGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7849
QY 7201 TCTGGGTAGGCAACATCATATGATGTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7260
Db 7850 TCTGGGTAGGCAACATCATATGATGTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7909
QY 7261 ACTCATTTCTTCCATCTTCTAGCTCAGGAAACCTTGAAAAAGCCCTAGATGTCAG 7320
Db 7910 ACTCATTTCTTCCATCTTCTAGCTCAGGAAACCTTGAAAAAGCCCTAGATGTCAG 7969
QY 7321 ATCTACGGGCGCTGTTACTCGATTGAGCGACTTGACCTACATCATGATCAATCAACGACTC 7380
Db 7970 ATCTACGGGCGCTGTTACTCGATTGAGCGACTTGACCTACATCATGATCAATCAACGACTC 8029
QY 7381 CATGGCTTAGGCAATTTTCACTTCATGATGATCTCTCCAGTGAATCAATAGGGTGGCT 7440
Db 8030 CATGGCTTAGGCAATTTTCACTTCATGATGATCTCTCCAGTGAATCAATAGGGTGGCT 8089
QY 7441 TCATGCTCAGGAACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAGT 7500
Db 8090 TCATGCTCAGGAACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAGT 8149

QY 7501 GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
Db 8150 GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTTC 8209
QY 7561 AACTGGGCAGTAAAGGACCAAGCTCAAACTCACTCAATCCCGGCTCCGCTCCAGTTGGAT 7620
Db 8210 AACTGGGCAGTAAAGGACCAAGCTCAAACTCACTCAATCCCGGCTCCGCTCCAGTTGGAT 8269
QY 7621 TTAATCCAGCTGGTTGTGTGCTGTTACAGCGGGGAGACATATATACAGGCTGTCTCGT 7680
Db 8270 TTAATCCAGCTGGTTGTGTGCTGTTACAGCGGGGAGACATATATACAGGCTGTCTCGT 8329
QY 7681 GCCCGACCCCGCTGGTTGTGTGCTGTTACAGCGGGGAGACATATATACAGGCTGTCTCGT 7740
Db 8330 GCCCGACCCCGCTGGTTGTGTGCTGTTACAGCGGGGAGACATATATACAGGCTGTCTCGT 8389
QY 7741 CTACTCCCCAACGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTTTT 7800
Db 8390 CTACTCCCCAACGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTTTT 8449
QY 7801 TTTCCC-----TT 7850
Db 8450 TTTCCCCTTTTTTCCCTTT 8509
QY 7851 TTTCCCTTTTTTTTTTCTCTTT 7910
Db 8510 CCCCCCTTTTTTCCCTTT 8569
QY 7911 TAGTCACGCTAGCTGTGAAGGTCGCTGAGCGGCTTGAGTCGAGAGTGTCTGATCTG 7970
Db 8570 TAGTCACGCTAGCTGTGAAGGTCGCTGAGCGGCTTGAGTCGAGAGTGTCTGATCTG 8629
QY 7971 GCCTCTCTCAGATCAAGT 7989
Db 8630 GCCTCTCTCAGATCAAGT 8648

RESULT 15

US-10-029-907-4
; Sequence 4, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8643
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)....(8407)
US-10-029-907-4

Query Match 90.4%; Score 7222.6; DB 4; Length 8643;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 7953; Conservative 0; Mismatches 24; Indels 676; Gaps 4;

QY 2 CCAGCCCCCGATTGGGGGAGACTCCACCATAGATCACTCCCTCTGTAGGAACTACTGT 61
Db 2 CCAGCCCCCGATTGGGGGAGACTCCACCATAGATCACTCCCTCTGTAGGAACTACTGT 61
QY 62 CTTACGAGAAAGCCTCTAGCCATCGCTTAGTATGATGCTGTCAGGCTCCAGACC 121
Db 62 CTTACGAGAAAGCCTCTAGCCATCGCTTAGTATGATGCTGTCAGGCTCCAGACC 121

QY	122	CCCCCTCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTCGCAGG	181	1190	AGACCACAAACGGTTTCCCTCTAGCGGGATCAATTCGGCCCTCTCCCTCCCCCCCCCCTA	1249
Db	122		181	1202	AGACCACAAACGGTTTCCCTCTAGCGGGATCAATTCG	1250
QY	182	ACGACCGGTCTCTTCTTGATCAACCCGCTCAATGCTTGGATTTGGCGGTGCCCGG	241	1250	ACGTTACTGGCCGAAGCCGCTTGGAAATAAGGCGGTGTCGTTGTCTATATGTTATTTT	1309
Db	182		241	1251	ACGTTACTGGCCGAAGCCGCTTGGAAATAAGGCGGTGTCGTTGTCTATATGTTATTTT	1310
QY	242	CGAGACTGTAGCCGAGTAGTGTGGGTCCGAAAGCCCTTGTGTAAGTGTGCTGATAGG	301	1310	CAACCATATGTCGCTCTTTTGGCAATGTGAGGCGCCGGAACCTGGCCCTGCTCTTGA	1369
Db	242		301	1311	CAACCATATGTCGCTCTTTTGGCAATGTGAGGCGCCGGAACCTGGCCCTGCTCTTGA	1370
QY	302	CGAGACTGTAGCCGAGTAGTGTGGGTCCGAAAGCCCTTGTGTAAGTGTGCTGATAGG	361	1370	CGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGTAAGTCTG	1429
Db	302		361	1371	CGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGTAAGTCTG	1430
QY	362	TGCTTCCGAGTGCCTCCGGAGGTCTCGTAGACCGCTGCACCATGAGCAGCAATCTTAACC	421	1430	TGAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACTGTGTAGCGACCCCTT	1489
Db	362		421	1431	TGAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACTGTGTAGCGACCCCTT	1490
QY	422	GCCTGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCACAAAGCAATTCGGCTGCTC	481	1490	GCAGGCGAGCGGAACCCCTTGGCGAAGGTGCTCTCGGCGCAAAAGCCAGCTGAT	1549
Db	422		481	1491	GCAGGCGAGCGGAACCCCTTGGCGAAGGTGCTCTCGGCGCAAAAGCCAGCTGAT	1550
QY	482	TGATGCCGCTGCTTCCGGCTGTGACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCGA	541	1550	AAGATACACCTGCAAGAGCGCGCAACCCAGTGTGTCAGTGTGATAGTGTG	1609
Db	482		541	1551	AAGATACACCTGCAAGAGCGCGCAACCCAGTGTGTCAGTGTGATAGTGTG	1610
QY	542	CCTGTCGCTGCTTCCGGCTGTGACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCGA	601	1610	AAAGGTCAAAATGCTCTCTCAAGCGTATTTCAACAAAGGGCTGAAGATGCCAGAGG	1669
Db	542		601	1611	AAAGGTCAAAATGCTCTCTCAAGCGTATTTCAACAAAGGGCTGAAGATGCCAGAGG	1670
QY	602	GACGGCGCTTCTTCCGAGCTGTGCTCGAGTGTGCTCAAGCGTATTTCAACAAAGGGCT	661	1670	TACCCCATTTGATGGGATCTGATCTGGGGCTCTGGTGACATCTTTACATGTTAGT	1729
Db	602		661	1671	TACCCCATTTGATGGGATCTGATCTGGGGCTCTGGTGACATCTTTACATGTTAGT	1730
QY	662	GCTATTGGCGAAGTCCCGGGCGAGGATCTCTGTCATCTACCTTGTCTTGGCGAGAA	721	1730	CGAGTTTAAACAAAGTCTAGGCGCCCGAAACACAGGGGACGTGGTGTTCCTTTTGA	1789
Db	662		721	1731	CGAGTTTAAACAAAGTCTAGGCGCCCGAAACACAGGGGACGTGGTGTTCCTTTTGA	1790
QY	722	AGTATCCATCATGGCTGATGCAATCGCGGCTGCATACGCTTGATTCGGCTACCTGCC	781	1790	ACGATAATACCATG	1803
Db	722		781	1791	ACGATAATACCATG	1850
QY	782	ATTTCGACCAACCAAGCGAATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGCT	841	1804	-----	1803
Db	782		841	1851	TGATATCTCTTGACCTTGTACCGCACATTAAGCTGTTCCTCGTAGGCTCATATGGTGT	1910
QY	842	TGTCGATCAGGATGTGGAAGAGCATCAGGGGCTCGCGCCAGCCGMACTGTCG	901	1804	-----	1803
Db	842		901	1911	TACAAATATTTATCACAGGGCGGAGGCACACTTGCAGTGTGATCCCCCCTCAACG	1970
QY	902	CAGGCTCAAGCGCGCATGCCGACGCGAGGATCTCGTGTGACCCATGGCGATGCCTG	961	1804	-----	1803
Db	902		961	1971	TTCCGGGGGCGCGGATCGGTCATCCTCTCACGTGCGGATCCACCCAGAGCTAATCT	2030
QY	962	CTTGCGCAATATCATGTGGAATAATGGCCCTTTTCTGGAATCATGACATGTGGCGGCT	1021	1804	-----	1803
Db	962		1021	2031	TTACCATCACCAAAATCTTGTCTGCCATACCTCGTCCACTCATGTGGTCTCCAGGCTGGA	2090
QY	1022	GGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCGCTCATATTCCTGAAGCT	1081	1804	-----	1803
Db	1022		1081	2091	TAAACAAAGTGCCTACTTCGTGGCGCACACGGGCTCATTCGTGCATGCTGTGTGTC	2150
QY	1082	TGGCGGGAATGGCTGACCTTCTCGTCTTTTACGGTATCGCCGCTCCCGATTCGCA	1141	1804	-----	1803
Db	1082		1141	2151	GGAAGTTGCTGGGGTCAATTAATGTCCAAATGGCTCTCATGAAGTTGGCCGCTACGAC	2210
QY	1142	GCGCATCGCCCTTCTATCGCTTCTTGAAGAGTCTTCTTGAGTCTTCTTGAGT	1189	1804	-----	1803
Db	1142		1189	2211	GTACGTAGTTTATGACCATCTACCCCACTGCGGGGACTGGGCCACCGGGCCCTACGAG	2270
				1804	-----	1803

Db	2271	ACCTTGCGGTGGCAGTTCAGCCCGTCTGCTCTCTCTGATATGAGACCAAGGTTATCACT	2330	3351	TCCTGGGATCGGCACAGTCTCTGGAACCAAGCGGAGACGGCTGGAGCGGACTCTGCTGCTGC	3410
QY	1804	-----	1803	2762	TCGCCACCGCTACGCTCCGGGATCGGTCACCGTGCACATCCCAAATCGAGGAGGTGG	2821
Db	2331	GGGGGGCAGACACCGCGCGTGTGGGACATCATCTTGGGCTGCCGCTCTCCGCCCGCA	2390	3411	TCGCCACCGCTACGCTCCGGGATCGGTCACCGTGCACATCCCAAATCGAGGAGGTGG	3470
QY	1804	-----	1803	2822	CTCTGTCCAGCAGTGGGAATCCCTTTTATGCAAGCCATCCCATCGAGCCATCA	2881
Db	2391	GGGGGGGAGATACATCTGGGACCGGCAGACAGCTTGAAGGCGAGGGTGGGACTCC	2450	3471	CTCTGTCCAGCAGTGGGAATCCCTTTTATGCAAGCCATCCCATCGAGCCATCA	3530
QY	1804	--GCGCCTATTACGCTTACTCCCAAACAGAGCGGAGGCTACTTGGCTGATCATCACTA	1861	2882	AGGGGGGAGGACCTCATTTTCTGCCATTTCCCAAGAAATGTGATGAGTTCGCGCGA	2941
Db	2451	TCGCGCTATTACGCTTACTCCCAAACAGAGCGGAGGCTACTTGGCTGATCATCACTA	2510	3531	AGGGGGGAGGACCTCATTTTCTGCCATTTCCCAAGAAATGTGATGAGTTCGCGCGA	3590
QY	1862	GCCTCAGAGCGCGGACAGGAACAGGTTCAGAGGGGAGGTCCAAAGTGGTCTCCACCGCAA	1921	2942	AGCTGTCGCGCTCGGACTCAATGCTGTAGCATATTAACCGGGGCTTGTATTCGCTCA	3001
Db	2511	GCCTCAGAGCGCGGACAGGAACAGGTTCAGAGGGGAGGTCCAAAGTGGTCTCCACCGCAA	2570	3591	AGCTGTCGCGCTCGGACTCAATGCTGTAGCATATTAACCGGGGCTTGTATTCGCTCA	3650
QY	1922	CACAACTTTTCCCTGGGACCTGGCTCAATGGCGTGTGGACTGTCTATCATGGTCCG	1981	3002	TACCAACTAGCGGAGAGCTGATGCTAGCAACGGAACGCTCTAATGACGGGCTTACCG	3061
Db	2571	CACAACTTTTCCCTGGGACCTGGCTCAATGGCGTGTGGACTGTCTATCATGGTCCG	2630	3651	TACCAACTAGCGGAGAGCTGATGCTAGCAACGGAACGCTCTAATGACGGGCTTACCG	3710
QY	1982	GCTCAAAGACCTTGCCTGGCCAAAGGCGCCAAATCACCCAAATGTACCAATGTGGAAC	2041	3062	GCATTTCCACTCAAGTATGCTGCAATACATGCTGACCCAGAGAGTGCATTCAGCC	3121
Db	2631	GCTCAAAGACCTTGCCTGGCCAAAGGCGCCAAATCACCCAAATGTACCAATGTGGAAC	2690	3711	GCATTTCCACTCAAGTATGCTGCAATACATGCTGACCCAGAGAGTGCATTCAGCC	3770
QY	2042	AGGACCTGCTGCGCTGGCAAGGCGCCCGCGGGCGGTTCTTGACACCATGACCTGCG	2101	3122	TGGAACCGACCTTCAACATTGAGACGACGACCGTGCACCAAGCGGGTGTACGCTCGC	3181
Db	2691	AGGACCTGCTGCGCTGGCAAGGCGCCCGCGGGCGGTTCTTGACACCATGACCTGCG	2750	3771	TGGAACCGACCTTCAACATTGAGACGACGACCGTGCACCAAGCGGGTGTACGCTCGC	3830
QY	2102	GACGCTCGGACCTTTACTTGGTTCAGAGGATGCGCATGTCAATTCGGTCCGCGCGCGG	2161	3182	AGCGGGGAGGAGGACTGATGAGGAGGATGGGCAATTTACAGGTTTGTGATCCAGGAG	3241
Db	2751	GACGCTCGGACCTTTACTTGGTTCAGAGGATGCGCATGTCAATTCGGTCCGCGCGCGG	2810	3831	AGCGGGGAGGAGGACTGATGAGGAGGATGGGCAATTTACAGGTTTGTGATCCAGGAG	3890
QY	2162	GGCAGACAGGGGGAGCTTACTCTCCCGCAGCGCGTCTCTACTTTGAAGGGCTCTTGG	2221	3242	AACGCGCTCTCGGCAATGTTCCGATTTCTTGGTCTGTCGAGTGTATGACGCGGCTGTG	3301
Db	2811	GGCAGACAGGGGGAGCTTACTCTCCCGCAGCGCGTCTCTACTTTGAAGGGCTCTTGG	2280	3891	AACGCGCTCTCGGCAATGTTCCGATTTCTTGGTCTGTCGAGTGTATGACGCGGCTGTG	3950
QY	2222	GCGGTCACTGCTCTGCGCTCGGGGACGCTGTGGGATCTTTTCGGGCTGCGGTGCA	2281	3302	CTTGTACGAGCTCAACGCGCGCGGAGCTCAGTTAGGTTGCGGCTTACCTTAACACAC	3361
Db	2871	GCGGTCACTGCTCTGCGCTCGGGGACGCTGTGGGATCTTTTCGGGCTGCGGTGCA	2930	3951	CTTGTACGAGCTCAACGCGCGCGGAGCTCAGTTAGGTTGCGGCTTACCTTAACACAC	4010
QY	2282	CCGAGGGGTTGCGAAGGGGTGACTTTGTACCCGTCAGTCTATGAAACCACTATGC	2341	3362	CAGGTTCCCGCTCTGCCAGGACCAATCTGGAGTTCTGGGAGAGCGCTTTTACAGGCTCA	3421
Db	2931	CCGAGGGGTTGCGAAGGGGTGACTTTGTACCCGTCAGTCTATGAAACCACTATGC	2990	4011	CAGGTTCCCGCTCTGCCAGGACCAATCTGGAGTTCTGGGAGGCGCTTTTACAGGCTCA	4070
QY	2342	GGTCCCGGCTTTCAGGACAACTCGTCCCTCCGCGCGTACCGCAGACATTCAGGTGG	2401	3422	CCCAATAGACGCGCAATTTCTTGTCCAGACTAAGCAGGAGGCTTTTACAGGCTCA	4070
Db	2991	GGTCCCGGCTTTCAGGACAACTCGTCCCTCCGCGCGTACCGCAGACATTCAGGTGG	3050	4071	CCCAATAGACGCGCAATTTCTTGTCCAGACTAAGCAGGAGGAGCAACTTCCCTTACC	4130
QY	2402	CCCATCTACGCGCCCTACTGGTAGCGGCAAGACACTAAGGTGCGGCTGCGTATGCG	2461	3482	TGTTAGCATACAGGCTACGCTGTCGCGGAGGCTCAGGCTTCCACCTCCCTGCGGAGC	3541
Db	3051	CCCATCTACGCGCCCTACTGGTAGCGGCAAGACACTAAGGTGCGGCTGCGTATGCG	3110	4131	TGTTAGCATACAGGCTACGCTGTCGCGGAGGCTCAGGCTTCCACCTCCCTGCGGAGC	4190
QY	2462	CCCAAGGTTAAGTGCTTCTCTGAAACCGTCCGTCGCGCCACCTAGGTTTCGGG	2521	3542	AAATGTGGAGTGTCTCATACGCTAAAGCTACGCTGACGCGGCAACGCGCTGTGT	3601
Db	3111	CCCAAGGTTAAGTGCTTCTCTGAAACCGTCCGTCGCGCCACCTAGGTTTCGGG	3170	4191	AAATGTGGAGTGTCTCATACGCTAAAGCTACGCTGACGCGGCAACGCGCTGTGT	4250
QY	2522	CGTATATGTCTAAGGCACTGATTCACCTTACATCAGACCGGGGTAAAGCACTCA	2581	3602	ATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCATAAACCAATACATCA	3661
Db	3171	CGTATATGTCTAAGGCACTGATTCACCTTACATCAGACCGGGGTAAAGCACTCA	3230	4251	ATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCATAAACCAATACATCA	4310
QY	2582	CCAGGCTGCCCCCATCAGTACTTCCACTATGGAAGTTTCTTCCGACGCTGGTGTCT	2641	3662	TGTCATGTCATGTCGGCTGACCTGGAGTGTCTACAGGAGCTTGGTGTGGTAGGCGAG	3721
Db	3231	CCAGGCTGCCCCCATCAGTACTTCCACTATGGAAGTTTCTTCCGACGCTGGTGTCT	3290	4311	TGTCATGTCATGTCGGCTGACCTGGAGTGTCTACAGGAGCTTGGTGTGGTAGGCGAG	3781
QY	2642	CTGGGCGCTTATGATCATATATGATGAGTGCCACTCAACTGATTCGACCACTA	2701	4371	TCTTAGCAGCTTGGCGGCTATGCTGACAAACAGGAGGCTGTCTTGTGGGAGGA	4430
Db	3291	CTGGGCGCTTATGATCATATATGATGAGTGCCACTCAACTGATTCGACCACTA	3350	3782	TCTATCTTGGGAAAGCGGCTCATTTCCCGAAGGGAAGTCTTTCACCGGAGTTGG	3841
QY	2702	TCTTGGGCACTCGGCACAGTCTCTGACCAAGCGGAGCGGCTGAGCGGAGCTGCTGTC	2761	4431	TCTATCTTGGGAAAGCGGCTCATTTCCCGAAGGGAAGTCTTTCACCGGAGTTGG	4490

Db 6651 CGGGCGCCTGATACGCCATCGCGTGGGAGGAACCAAGTGCCTCAATCAATGCACTGA 6710
QY 6062 GCAACTCTTTGCTCGGTCAACAACTTTGGTCTATGCTTACAACTCTCGAGCGCAAGCC 6121
Db 6711 GCAACTCTTTGCTCGGTCAACAACTTTGGTCTATGCTTACAACTCTCGAGCGCAAGCC 6770
QY 6122 TGGGCGAGAGAGGTCACTCTTTCACAGACTGCGAGTCTCGAGCAAGCCACTACCGGAGC 6181
Db 6771 TGGGCGAGAGAGGTCACTCTTTCACAGACTGCGAGTCTCGAGCAAGCCACTACCGGAGC 6830
QY 6182 TGCTCAAGGAGATGAAGCGAGCGGTCCACAGTTTAAAGCTTAAAGCTTCTATCCGTGGAGG 6241
Db 6831 TGCTCAAGGAGATGAAGCGAGCGGTCCACAGTTTAAAGCTTAAAGCTTCTATCCGTGGAGG 6890
QY 6242 AAGCCTGTAGCTGAGCGGCCCAATTCGGCCAGATCTAAATTTGGCTATGGGGCAAGG 6301
Db 6891 AAGCCTGTAGCTGAGCGGCCCAATTCGGCCAGATCTAAATTTGGCTATGGGGCAAGG 6950
QY 6302 ACGTCCGGAACTTATCCAGCAAGCGGTTTAAACACATTCGGTCTCGGTGTGGAAGSACTTGC 6361
Db 6951 ACGTCCGGAACTTATCCAGCAAGCGGTTTAAACACATTCGGTCTCGGTGTGGAAGSACTTGC 7010
QY 6362 TGAAGACACTGAGACACCAATTTGACACCACTCATGCGCAAAATAGAGTTTCTGCG 6421
Db 7011 TGAAGACACTGAGACACCAATTTGACACCACTCATGCGCAAAATAGAGTTTCTGCG 7070
QY 6422 TCCAAACAGAGAGGGGGCGGCAAGCCAGCTCGCCTTATCGTATTCCTCAAGATTTGGGG 6481
Db 7071 TCCAAACAGAGAGGGGGCGGCAAGCCAGCTCGCCTTATCGTATTCCTCAAGATTTGGGG 7130
QY 6482 TTGCTGTGTGCGAGAAATGGCCCTTTTACGATGTGCTTCCACCTCTCCAGCGGTGA 6541
Db 7131 TTGCTGTGTGCGAGAAATGGCCCTTTTACGATGTGCTTCCACCTCTCCAGCGGTGA 7190
QY 6542 TGGGCTCTTTATACGATTTCCAAATCTCTCTGAGAGGCTTACCAATGTTGTGACTTGGGCC 6601
Db 7191 TGGGCTCTTTATACGATTTCCAAATCTCTCTGAGAGGCTTACCAATGTTGTGACTTGGGCC 7250
QY 6602 CTGGAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCGGCTGTTTGTGACTCAA 6661
Db 7251 CTGGAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCGGCTGTTTGTGACTCAA 7310
QY 6662 CGGTCACTGAGATGACATCCGTTGTGAGAGTCAATCTACCAATGTTGTGACTTGGGCC 6721
Db 7311 CGGTCACTGAGATGACATCCGTTGTGAGAGTCAATCTACCAATGTTGTGACTTGGGCC 7370
QY 6722 CCGAAGCCAGACAGGCCATAGGTGCTTCAAGAGCGGCTTACATCGGGGGCCCCCTGA 6781
Db 7371 CCGAAGCCAGACAGGCCATAGGTGCTTCAAGAGCGGCTTACATCGGGGGCCCCCTGA 7430
QY 6782 CTAATTTCTAAGGGAGAACTGCGGCTATCGCGGTATCGCGGCGAGCGGTGTACTGAGCA 6841
Db 7431 CTAATTTCTAAGGGAGAACTGCGGCTATCGCGGTATCGCGGCGAGCGGTGTACTGAGCA 7490
QY 6842 CCAGTCGGGTAAATACCTCTACATGTTTACTTGAAGCGCGTGTGCGGCTGTGCGACTGCGA 6901
Db 7491 CCAGTCGGGTAAATACCTCTACATGTTTACTTGAAGCGCGTGTGCGGCTGTGCGACTGCGA 7550
QY 6902 AGCTCCAGGACTGACAGTGTCTGTATGCGGAGAGCGCTTGTGCTTATCTGTGAAAGCG 6961
Db 7551 AGCTCCAGGACTGACAGTGTCTGTATGCGGAGAGCGCTTGTGCTTATCTGTGAAAGCG 7610
QY 6962 CGGGGACCCAAAGAGGAGCGAGCGGCTTACGGGCTTCAAGGAGGCTATGACTAGATACT 7021
Db 7611 CGGGGACCCAAAGAGGAGCGAGCGGCTTACGGGCTTCAAGGAGGCTATGACTAGATACT 7670
QY 7022 CTGCCCCCTGGGAGCGGCCCAACAGATACGACTTGGAGTTGATAACATCATGCT 7081
Db 7671 CTGCCCCCTGGGAGCGGCCCAACAGATACGACTTGGAGTTGATAACATCATGCT 7730
QY 7082 CCTCCAAATGTGTGAGTGGCGCAGATGCTGCAAAAGGTTGACTATCTCACCGGTTG 7141

Db 7731 CCTCCAAATGTGTGAGTGGCGCAGATGCTGCGAAAGGGTGTACTATCTCACCCGTTG 7790
QY 7142 ACCCCACACCCCCCTTTCGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAATT 7201
Db 7791 ACCCCACACCCCCCTTTCGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAATT 7850
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Search completed: November 2, 2004, 07:21:45
Job time : 676 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 1, 2004, 16:41:32 ; Search time 14582 Seconds
(without alignments)
19971.632 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	794	9.9	804	7	CK291519
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5	794	9.9	933	7	CK291799
6	794	9.9	936	7	CK256977
7	794	9.9	947	7	CK298208
8	794	9.9	954	7	CK283361
9	778.8	9.7	811	7	CK288185
10	587	7.3	878	7	CK288711
11	577.4	7.2	789	8	AQ361914
12	559.8	7.0	620	8	AQ398387
13	542.4	6.8	549	8	CK801630
14	514.8	6.4	561	8	AQ447874
15	508	6.4	509	8	AQ447775
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17	503.8	6.3	592	8	AQ449162
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24	468.8	5.9	594	8	AQ397253

C 25	465.2	5.8	850	8	AQ875052
C 26	463.4	5.8	798	8	AQ876139
C 27	458.8	5.7	482	1	AL449872
C 28	456.8	5.7	861	8	AQ875040
C 29	455.6	5.7	815	8	AQ876134
C 30	451.2	5.6	799	8	AQ876220
C 31	450	5.6	784	8	AQ876152
C 32	444.6	5.6	790	8	AQ875904
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C 38	409.4	5.1	748	8	AQ501530
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C 40	408	5.1	656	8	AQ447140
C 41	404	5.1	790	8	AQ875912
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ALIGNMENTS

CK284786 935 bp mRNA linear EST 02-AUG-2004
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normalized, full-length Nicotiana benthamiana cDNA clone NEMAQ41 5',
end, mRNA sequence.
CK284786 GI:39858698
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 935)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST747509
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

Location/Qualifiers
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/db_xref="taxon:4100"
/clone="NEMAQ41"
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callus tissue and root tissue"
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/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from


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QY 1049 AGCGTTGTGCTACCGCTGATATGCTGAAGAGCTTGGCGGCGAATGGCTTCTCT 1108
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QY 1109 CGTCTTTACGATTCGCGGCTCCCGATTCGAGCGCATCGCTTCTATCGCCTTCTTGA 1168
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end, mRNA sequence.
CK287297
CK287297.1 GI:39863696
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 856)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST750020
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
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challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 9.9%; Score 794; DB 7; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.8e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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LOCUS
DEFINITION
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EST750652 Nicotiana benthamiana mixed tissue cDNA library.
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normalized, full-length Nicotiana benthamiana cDNA clone NEMBC75 5'

end, mRNA sequence.

CK287930

CK287930.1 GI:39864940

EST.

Nicotiana benthamiana

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 910)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST750653

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics Institute via <http://genome.arizona.edu/orders/>

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

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ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 910;

Best Local Similarity 100.0%; Pred. No. 3.8e-174;

Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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4 GATTGAACAGATGATGACGAGGTTCTCCGGCCGCTGGTGGAGAGGCTATTCCG 63

449 CTATGACTGGGCAACAGCAATCGCTGCTGATGCCCGCGTTCCGGCTGTACGC 508

64 CTATGACTGGGCAACAGCAATCGCTGCTGATGCCCGCGTTCCGGCTGTACGC 123

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CK291799 933 bp mRNA linear EST 02-AUG-2004

CK291799

LOCUS

EST754513 Nicotiana benthamiana mixed tissue cDNA library,

normalized, full-length Nicotiana benthamiana cDNA clone NEMC477 5'

end, mRNA sequence.

CK291799

CK291799.1 GI:39872608

EST.

KEYWORDS

SOURCE

Nicotiana benthamiana

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.

1 (bases 1 to 933)

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Other ESTs: EST754514

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics Institute via <http://genome.arizona.edu/orders/>

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

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FEATURES

source

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

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Query Match      9.9%; Score 794; DB 7; Length 933;
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QY 706 AGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCCT 765
DB |||||
QY 1109 CGTGTCTTACGGTATCGCGCTCCGATTCGCGAGCGCATCGCTTCTATCGCCTTCTTGA 1168
DB |||||
QY 766 CGTGTCTTACGGTATCGCGCTCCGATTCGCGAGCGCATCGCTTCTATCGCCTTCTTGA 825
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QY 1169 CGAGTTCTTCTGAG 1182
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QY 826 CGAGTTCTTCTGAG 839
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RESULT 6

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CK256977
LOCUS
DEFINITION
CK256977 936 bp mRNA linear EST 30-JUL-2004
Solanum tuberosum cDNA library, normalized and full-length
CK256977
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 936)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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Location/Qualifiers
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full-length"
/note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

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ORIGIN

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Query Match      9.9%; Score 794; DB 7; Length 936;
Best Local Similarity 100.0%; Pred. No. 3.9e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||
QY 449 CTATGACTGGGCACACAGCAATCGGCTGCTCTGATGCCCGCGTTCCTCGGCTGTGCG 508
DB |||||
QY 74 CTATGACTGGGCACACAGCAATCGGCTGCTCTGATGCCCGCGTTCCTCGGCTGTGCG 133
DB |||||
QY 509 GCAGGGGCGCGGTTCTTTTGTCAAGACCGGAGTGTGCGGCGCTTTCCTTGGCAGCTGTGCT 628
DB |||||
QY 134 GCAGGGGCGCGGTTCTTTTGTCAAGACCGGAGTGTGCGGCGCTTTCCTTGGCAGCTGTGCT 253
DB |||||
QY 569 GAGACGAGCAGCGCGCTATCGTGGCTGGCCACGACGCGGCGTTCCTTGGCAGCTGTGCT 688
DB |||||
QY 194 GAGACGAGCAGCGCGCTATCGTGGCTGGCCACGACGCGGCGTTCCTTGGCAGCTGTGCT 253
DB |||||
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DB |||||
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DB |||||
QY 689 TCTCTGTCTATCTACCTTGTCTCTCGGAGAAAGTATCCATCATGCTGCTGATGCAATGCG 748
DB |||||
QY 314 TCTCTGTCTATCTACCTTGTCTCTCGGAGAAAGTATCCATCATGCTGCTGATGCAATGCG 373
DB |||||
QY 749 GCGGCTGTGATACGCTTGTATCCCGGCTACCTGCCCATTCGACCAAGCGGAAATCGCAT 808
DB |||||
QY 374 GCGGCTGTGATACGCTTGTATCCCGGCTACCTGCCCATTCGACCAAGCGGAAATCGCAT 433
DB |||||

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 869 GCATCAGGGGCTCGGCGCAGCCGAACCTGTTCCCGAGGCTCAAGGCGCGCATCCCGACGG 928
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 554 CGAGGATCTGTCGTCGACCCATGCGGATCGCTTTCGCGATATCATGCTGGAATCG 613
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 1169 CGAGTTCTTCTGAG 1182
 794 CGAGTTCTTCTGAG 807

RESULT 7
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 EST760922 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NEMDE30 5'
 end, mRNA sequence.

CK298208
 CK298208.1 GI:39885354
 EST.

Accession
 Version
 Keywords
 Source
 Organism
 Nicotiana benthamiana
 Nicotiana benthamiana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Nicotiana.

Reference
 Authors
 Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
 Skaskiewicz, B., Jin, H. and Baker, B.
 Generation of EST sequences from Nicotiana benthamiana
 Unpublished (2003)
 Other ESTs: EST760923

Title
 Journal
 Comment
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from the University of Arizona Genomics
 Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.
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 /lab_host="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Nicotiana benthamiana
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr);

Xanthomonas campestris pv campestris 12 hr, 18hr;
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
 campestris pv vesicatoria 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

ORIGIN
 Query Match 9.9%; Score 794; DB 7; Length 947;
 Best Local Similarity 100.0%; Pred. No. 3.9e-174; Indels 0; Gaps 0;
 Matches 794; Conservative 0; Mismatches 0;
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 17 GATTGAACAAGATGATTGACGAGGTTCTCCGCGCTTGGGTGGAGAGGCTATTCGG 76
 449 CTATGACTGGGCACAAACAGCAATCGGCTGCTCTGATGCCGCGTCTTCGGCTGTGCG 508
 77 CTATGACTGGGCACAAACAGCAATCGGCTGCTCTGATGCCGCGTCTTCGGCTGTGCG 136
 509 GAGGGGCGCGCGGTTCTTTTGTCAAGACCGACCTGTCGGTGGCCCTGAACTGAATGCA 568
 137 GCAGGGGCGCGCGGTTCTTTTGTCAAGACCGACCTGTCGGTGGCCCTGAACTGAATGCA 196
 569 GAGGAGGCGAGCGCGCTATCGTGGCTGGCCACGAGCGGCGTTCCTTGGCAGCTGTGCT 628
 197 GAGGAGGCGAGCGCGCTATCGTGGCTGGCCACGAGCGGCGTTCCTTGGCAGCTGTGCT 256
 629 CGACGTTGTCACTGAAGCGGGAAGGAGTGGTGTCTATTGGGGGAAGTGGCGGGGAGGA 688
 257 CGACGTTGTCACTGAAGCGGGAAGGAGTGGTGTCTATTGGGGGAAGTGGCGGGGAGGA 316
 689 TCTCCTGTCTATCTACTTCTCTCCGAGAAAGTATCCATCATGCTCATGCAATGCG 748
 317 TCTCCTGTCTATCTACTTCTCTCCGAGAAAGTATCCATCATGCTCATGCAATGCG 376
 749 GCGGCTGCATACGTTGATCGGCTACTCCCATTCGACCAACGAGCGAAACATCGCAT 808
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 437 CGAGGAGCAGCTACTCGGATGGAAGCCGGTCTTGTCTGATCAGGATGATCTGACGAAGA 496
 869 GCATCAGGGGCTCGGCGCAGCCGAACCTGTTCCCGAGGCTCAAGGCGCGCATGCCCGAGG 928
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 929 CGAGGATCTCGTCTGACCCATGCGGATCGCTGCTTCCGGAATATCATGTTGGAATGG 988
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 989 CCGCTTTTCTGATTCATCGACTGTGCGCGGCTGGGTGTGGCGACCGCTATCAGGACAT 1048
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 1049 AGCGTTGGCTACCGCTGATATGCTGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCT 1108
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 1109 CGTGTCTTACGATCGCGCTCCGATTCGAGCGCATGCGCTTCTATCGCTTCTTGA 1168
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 1169 CGAGTTCTTCTGAG 1182
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 EST746083 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NEMAG50 5'


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end, mRNA sequence.
ACCESSION CK283361
VERSION CK283361.1 GI:39855898
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 (bases 1 to 954) asterids; lamids; Solanales; Solanaceae; Nicotiana.
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST746084
Contact: Robin Buell
7912 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
ORIGIN
Query Match 9.9%; Score 794; DB 7; Length 954;
Best Local Similarity 100.0%; Pred. No. 3.9e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 GATTGAACAAAGATGGATTGACGAGGTTCTCCGGCGCTTGGGTGGAGAGGCTATTTCGG 448
DB 14 GATTGAACAAAGATGGATTGACGAGGTTCTCCGGCGCTTGGGTGGAGAGGCTATTTCGG 73
QY 449 CTATGACTGGGACACACAGACATCGCTGCTGTGATGCCGCGTTCGGGTGTCAGC 508
DB 74 CTATGACTGGGACACACAGACATCGCTGCTGTGATGCCGCGTTCGGGTGTCAGC 133
QY 509 GCAGGGGGCCCGCGTCTTTTCTCAAGACCGACCTCGCGTCCGCTCAATGAATGCA 568
DB 134 GCAGGGGGCCCGCGTCTTTTCTCAAGACCGACCTCGCGTCCGCTCAATGAATGCA 193
QY 569 GGACGAGGCGCGCGCTATCGTGGTGGCCACGCGGCTTCCTTGGCGAGCTGTGCT 628
DB 194 GGACGAGGCGCGCGCTATCGTGGTGGCCACGCGGCTTCCTTGGCGAGCTGTGCT 253
QY 629 CGACGTTGTCATGAAGCGGAGGAGCTGGGTGCTATTGGGCGAAGTCCCGGGCAGGA 688
DB 254 CGACGTTGTCATGAAGCGGAGGAGCTGGGTGCTATTGGGCGAAGTCCCGGGCAGGA 313
QY 689 TCTCTGTCATCTCACTTGTCTTCCCGGAGAAAGTATCCATCATGCTGATGCAATGG 748
DB 314 TCTCTGTCATCTCACTTGTCTTCCCGGAGAAAGTATCCATCATGCTGATGCAATGG 373

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QY 749 GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTGCAACCAAGCGAAACATCGCAT 808
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QY 809 CGAGCGACAGCTACTCGGATGGAGCCGCTCTTCTGATCAGGATGATCTGGACGAGA 868
DB 434 CGAGCGACAGCTACTCGGATGGAGCCGCTCTTCTGATCAGGATGATCTGGACGAGA 493
QY 869 GCATCAGGGCTCGCGCCAGCCGCAACTCTTCGCCAGGCTCAAGGCGCCATGCCGACGG 928
DB 494 GCATCAGGGCTCGCGCCAGCCGCAACTCTTCGCCAGGCTCAAGGCGCCATGCCGACGG 553
QY 929 CGAGGATCTCGTGTGACCCATGCGGATGCTGCTTCCGGAATATCATGGTGGAAATGG 988
DB 554 CGAGGATCTCGTGTGACCCATGCGGATGCTGCTTCCGGAATATCATGGTGGAAATGG 613
QY 989 CCGCTTTCTCGATTTCATCGACTGCGCGCTGGGTGTGGCGACCGCTATCAGGACAT 1048
DB 614 CCGCTTTCTCGATTTCATCGACTGCGCGCTGGGTGTGGCGACCGCTATCAGGACAT 673
QY 1049 AGCGTTGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCT 1108
DB 674 AGCGTTGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCT 733
QY 1109 GGTGCTTACGATTCGCGCTCCGATTCGAGCGATTCGAGCGATTCGATCGCCTTCTTGA 1168
DB 734 GGTGCTTACGATTCGCGCTCCGATTCGAGCGATTCGAGCGATTCGATCGCCTTCTTGA 793
QY 1169 CGAGTTCTTCTGAG 1182
DB 794 CGAGTTCTTCTGAG 807
CK288185 811 bp mRNA linear EST 02-AUG-2004
EST750907 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMB61 5'
end, mRNA sequence.
CK288185
CK288185.1 GI:39865462
EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 811)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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callus tissue and root tissue"
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library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana

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tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN	Query Match		9.7%; Score 778.8; DB 7; Length 811;		Best Local Similarity 99.7%; Pred. No. 1.3e-170;		Matches 780; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
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QY	386	CATGATTGAACAGATGGAATCCACGAGGTTCTCGGCGCTTGGGTGGAGAGGCTATT	445					
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QY	446	CGGCTATGACTGGCACACACACATCGCTGCTGATGCGCGCTTCCGGCTGC	505					
	90	CGGCTATGACTGGCACACACACATCGCTGCTGATGCGCGCTTCCGGCTGC	149					
QY	506	ACGCGAGGGCGCCCGCTTTCTTTTCTCAAGACCGACCTGTCCGGTSCCTCGAATGAAT	565					
	150	ACGCGAGGGCGCCCGCTTTCTTTTCTCAAGACCGACCTGTCCGGTSCCTCGAATGAAT	209					
QY	566	GCAGGACGAGGCGCGGCTATGCTGGTGGCCACGAGGGGTTCTTGGCGACTGT	625					
	210	GCAGGACGAGGCGCGGCTATGCTGGTGGCCACGAGGGGTTCTTGGCGACTGT	269					
QY	626	GCTCGAGCTGTCACTGAAGCGGAGGAGGACTGGCTGCTATTGGCGGAAGTCCGGGCA	685					
	270	GCTCGAGCTGTCACTGAAGCGGAGGAGGACTGGCTGCTATTGGCGGAAGTCCGGGCA	329					
QY	686	GGATCTCTGTCATCTCACCTTGCTCTGCGCGAGAAAGTATCCATCATGCTCATGCAAT	745					
	330	GGATCTCTGTCATCTCACCTTGCTCTGCGCGAGAAAGTATCCATCATGCTCATGCAAT	389					
QY	746	CGCGCGGCTGCATACCGTTGATCGGTTGATCGGCTTCTGCGCCATTCGACCAACGAAACATCG	805					
	390	CGCGCGGCTGCATACCGTTGATCGGTTGATCGGCTTCTGCGCCATTCGACCAACGAAACATCG	449					
QY	806	CATCGAGCAGCAGCTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGACGA	865					
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QY	866	AGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCGAGGCTCAAGCGCGCATGCCGA	925					
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	630	TGGCGGCTTTCTGATTCATGCTGCTGCGGCTGCGGCTGCTGCGGACCGCTATCAGGA	689					
QY	1046	CATAGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGCGGAATGGGCTGACCGCTT	1105					
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QY	1106	CCTCGTGTTCAGGTATCGGCTCCCGATTCGAGCGGATCGCTTCTATCGCCTTCT	1165					
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QY	1166	TG 1167						
	810	TG 811						

CK288711 878 bp mRNA linear EST 02-AUG-2004
EST751433 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NEMBI49 5' end, mRNA sequence.
CK288711 GI:39866496
EST.
CK288711.1
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 878)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
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/clone="NEMBI49"
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/lab_host="DH10B-TonA"
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/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match		7.3%; Score 587; DB 7; Length 878;		Best Local Similarity 100.0%; Pred. No. 9.3e-126;		Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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656		CTGCTGCTATTGGCGGAAGTGGCGGCGAGGATCTCTGTCATCTCACTTGTCTCTTC	715				
61		CTGCTGCTATTGGCGGAAGTGGCGGCGAGGATCTCTGTCATCTCACTTGTCTCTTC	120				
716		CGAGAAAGTATCCATCATGCTGATGCAATGCGGCGTGCATACGCTTGTATCCGGCTAC	775				
121		CGAGAAAGTATCCATCATGCTGATGCAATGCGGCGTGCATACGCTTGTATCCGGCTAC	180				
776		CTGCCCATTCGACCAACCAACATCGCATCGAGCAGCAGTACTCGATCGGAAGC	835				
181		CTGCCCATTCGACCAACCAACATCGCATCGAGCAGCAGTACTCGATCGGAAGC	240				
836		CGGTCTTGTGATCAGGATGATCTGGACGAAGAGATCAGGGGCTCGGCGCGGAAC	895				
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QY 896 GTTCGCCAGGCTCANGCGCGCATGCCGACGCGGAGGATCTCGTGTGACCCCATGCCGA 955
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QY 956 TGCCTGCTTCCGGAATATCATGCTGAAATGCGCGCTTTCTTGGATTTCATCGACTGTGG 1015
Db 361 TGCCTGCTTCCGGAATATCATGCTGAAATGCGCGCTTTCTTGGATTTCATCGACTGTGG 420
QY 1016 CCGGCTGGGTGGCGGACCGGTATCAGGACATAGCGTTGGTACCCGTGATATGCTGA 1075
Db 421 CCGGCTGGGTGGCGGACCGGTATCAGGACATAGCGTTGGTACCCGTGATATGCTGA 480
QY 1076 AGAGCTTGGCGGGAATGGGCTGACCGCTTCTCGTCTTACGGTATCGCGCTCCCGA 1135
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QY 1136 TTCCGAGCGCATGCGCTTCTATCGCTTCTTACGAGTTCTTCTGAG 1182
Db 541 TTCCGAGCGCATGCGCTTCTATCGCTTCTTACGAGTTCTTCTGAG 587

RESULT 11
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  clone mgxb0005K01f, genomic survey sequence.
ACCESSION
  AQ361914
VERSION
  AQ361914.1 GI:4211753
KEYWORDS
  GSS.
SOURCE
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  Magnaporthe grisea
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
  1 (bases 1 to 789)
  Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
  Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
  A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
  Genome
  Unpublished (1998)
  Contact: Dean RA
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson University, Clemson, SC 29634
  Tel: 864 656 5737
  Fax: 864 656 4293
  Email: rdean@clemson.edu
  Seq primer: TAATACGACTCTATATAGGG
  Class: BAC ends
  High quality sequence start: 41
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      /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
      Rice blast is one of the most devastating fungal diseases
      of rice world wide. It is a filamentous ascomycete with
      a haploid genome (n=7) of approximately 40 Mbp. Rice
      blast is an important model fungal pathogen for studying
      numerous aspects of the fungal-host interaction. In
      order to facilitate genome wide analysis, a BAC library
      containing 9216 clones with an average insert size of 130
      kbp was constructed. This library represents greater
      than 25X genome coverage. High density colony filters
      are available upon request."

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Query Match 7.2%; Score 577.4; DB 8; Length 789;
Best Local Similarity 97.8%; Pred. No. 1.6e-123;
Matches 584; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 581 GCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGGCAGCTGTGCTCGAGCTTCTCAC 640
Db 39 GCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGGCAGCTGTGCTCGAGCTTCTCAC 98
QY 641 TGAAGCGGGAAGGAGTGTGCTCTATTGGGCGAAGTTCGCGGGGCGAGGATCTCTGTCTATC 700
Db 99 TGAAGCGGGAAGGAGTGTGCTCTATTGGGCGAAGTTCGCGGGGCGAGGATCTCTGTCTATC 158
QY 701 TCACCTTGTCTCTCCGCGAGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGTGATAC 760
Db 159 TCACCTTGTCTCTCCGCGAGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGTGATAC 218
QY 761 GCTTGATCCGGCTACCTGCTCCCATTCGACCCACCAAGCGAAACATCGCATCGAGGAGCAG 820
Db 219 GCTTGATCCGGCTACCTGCTCCCATTCGACCCACCAAGCGAAACATCGCATCGAGGAGCAG 278
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QY 941 CGTGACCATGCGGATGCTGCTTGGCGAATATCATGCTGGAAATGCGCGCTTCTTCGG 1000
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QY 1001 ATTTCATGACTGTGCGCGCTGGGTGGCGGACCGCTATCAGGACATAGCGTTGGCTAC 1060
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QY 1061 CCGTGATATTGCTCAAGAGCTTGGCGGGAATGGGCTGACCGCTTCTCGTGTTCAGG 1120
Db 519 CCGTGATATTGCTCAAGAGCTTGGCGGGAATGGGCTGACCGCTTCTCGTGTTCAGG 578
QY 1121 TATCGCGCTCCCGATTGCGAGCGCATGCGCTTCTATCGGCTTCTTACGAGTTCTT 1177
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RESULT 12
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LOCUS
DEFINITION
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  clone mgxb0009J05f, genomic survey sequence.
ACCESSION
  AQ398387
VERSION
  AQ398387.1 GI:4369414
KEYWORDS
  GSS.
SOURCE
  Magnaporthe grisea (anamorph: Pyricularia grisea)
  Magnaporthe grisea
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  Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
  1 (bases 1 to 620)
  Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
  Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
  A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
  Genome
  Unpublished (1998)
  Contact: Dean RA
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson University, Clemson, SC 29634
  Tel: 864 656 5737
  Fax: 864 656 4293
  Email: rdean@clemson.edu
  Seq primer: TAATACGACTCTATATAGGG
  Class: BAC ends
  High quality sequence stop: 187.

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/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

CK801630 GI:43400943
EST.
Schedonorus arundinaceus (Festuca arundinacea)
Schedonorus arundinaceus
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poaceae; Schedonorus.
1 (bases 1 to 549)
Zhang, Y., Zwonitzer, J.C., Chekhovskiy, K., May, G.D. and Mian, M.A.R.
A functional genomics approach for identification of heat tolerance
genes in tall fescue
(in) Hopkins, A., Wang, Z.Y., Mian, R., Sledge, M. and Barker, R.R.
(eds.), MOLECULAR BREEDING OF FORAGE AND TURF, Kluwer Acad. Pub. 0,
87-96 (2003)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Rouf Mian (rmian@nobel.org) regarding clone availability
Seq primer: M13 reverse primer
High quality sequence stop: 470.

FEATURES source

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ORIGIN

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Matches 543; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 676 TGCCGGGCGAGGATCTCTGTCTCATCTCACCCTGTCTTCCGCGAGAAATATCATATG 735
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Qy 736 CTGATGCAATCGCGCGGTGATCGTGTGATCGGCTACCTGCCATTCGACCAACCAAG 795
Db 186 CTGATGCAATCGCGCGGTGATCGTGTGATCGGCTACCTGCCATTCGACCAACCAAG 245
Qy 796 CGAAACATCGCATCGAGCGACGCTACTCGATGGAAGCGGTCTTGTTCGATCAGGATG 855
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Qy 856 ATCTCGACGAGAGCATCAGGGGCTCGCGCCACGCGAACTGTTCGCGAGGCTCAAGCGGC 915
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Qy 916 GCATGCCGACGCGGAGGATCTCGTGTGACCCATGGCGATCGCTGCTTCCGAAATATCA 975
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7.0%; Score 559.8; DB 8; Length 620;
Query Match 98.8%; Pred. No. 2e-119; Indels 0; Gaps 0;
Matches 564; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 609 GTTCTTGGCAGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668
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Qy 1029 CGGACCGCTATCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1088
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CK801630 549 bp mRNA linear EST 26-FEB-2004
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QY      1096  CTGA 1099
Db      546  CTGA 549

RESULT 14
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VERSION    AQ447874.1 GI:4577011
KEYWORDS   GSS.
SOURCE     Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM   Magnaporthe grisea
REFERENCE  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS    Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
TITLE      1 (bases 1 to 561)
JOURNAL    Yu, Y.; Zhu, H.; Boyd, C.A.; Gaudette, B.; Gayle, A.; Kingsbury, R.;
COMMENT    Phillips, K.; Sasnowski, M.; Wing, R.A. and Dean, R.A.
           A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
           Genome
           Unpublished (1998)
           Contact: Dean RA
           Clemson University Genomics Institute
           100 Jordan Hall, Clemson University, Clemson, SC 29634
           Tel: 864 656 5737
           Fax: 864 656 4293
           Email: rdean@clemson.edu
           Seq primer: TAATACGACTCCTATAGGG
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               Rice blast is one of the most devastating fungal diseases
               of rice world wide. It is a filamentous ascomycete with
               a haploid genome (n=7) of approximately 40 Mbp. Rice
               blast is an important model fungal pathogen for studying
               numerous aspects of the fungal-host interaction. In
               order to facilitate genome wide analysis, a BAC library
               containing 9216 clones with an average insert size of 130
               kbp was constructed. This library represents greater
               than 25X genome coverage. High density colony filters
               are available upon request."

FEATURES
source
  Query Match 6.4%; Score 514.8; DB 8; Length 561;
  Best Local Similarity 99.6%; Pred. No. 6.4e-109;
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QY      870  CATAGGGGCTCGCGCCAGCCGAACCTGTTCCGAGGCTCAAGCGCGCATGCCGACGCG 929
Db      404  CATAGGGGCTCGCGCCAGCCGAACCTGTTCCGAGGCTCAAGCGCGCATGCCGACGCG 463
QY      930  GAGGATCTCTGCTGACCCCATGGCGATGCTGCTTGGCGAATATCATGTTGAAAATGSC 989
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QY      990  CGCTTTTCTGGATTTCATCGACTGTGGCGGCTGGGTGT 1027
Db      524  CGCTTTTCTGGATTTCATCGACTGTGGCGGCTGGGTGT 561

RESULT 15
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DEFINITION  clone mgxb0011E13f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
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VERSION    AQ447775.1 GI:4576912
KEYWORDS   GSS.
SOURCE     Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM   Magnaporthe grisea
REFERENCE  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS    Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
TITLE      1 (bases 1 to 509)
JOURNAL    Yu, Y.; Zhu, H.; Boyd, C.A.; Gaudette, B.; Gayle, A.; Kingsbury, R.;
COMMENT    Phillips, K.; Sasnowski, M.; Wing, R.A. and Dean, R.A.
           A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
           Genome
           Unpublished (1998)
           Contact: Dean RA
           Clemson University Genomics Institute
           100 Jordan Hall, Clemson University, Clemson, SC 29634
           Tel: 864 656 5737
           Fax: 864 656 4293
           Email: rdean@clemson.edu
           Seq primer: TAATACGACTCCTATAGGG
           Class: BAC ends
           High quality sequence stop: 342.
           Location/Qualifiers
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               Rice blast is one of the most devastating fungal diseases
               of rice world wide. It is a filamentous ascomycete with

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Tue Nov 2 14:02:18 2004

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

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Query Match          6.4%; Score 508; DB 8; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.4e-107;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 689 TCTCCTGTCACTCACTACCTTGTCTCCGCGAGAAAGTATCCATCATGGCTGATGCAATGCG 748
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QY 749 GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAACCAAGCGAAACATCGCAT 808
Db 121 GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAACCAAGCGAAACATCGCAT 180

QY 809 CGAGCGAGACGCTACTCGGATGGAAGCGGCTTTGTGATCAGGATGATCTGGACGAAGA 868
Db 181 CGAGCGAGACGCTACTCGGATGGAAGCGGCTTTGTGATCAGGATGATCTGGACGAAGA 240

QY 869 GCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCGAGCTCAAGCGCGCATGCCCGACGG 928
Db 241 GCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCGAGCTCAAGCGCGCATGCCCGACGG 300

QY 929 CGAGGATCTCGTGTGACCCATGCGGATGCTGCTGCCGAATATCATGTGGAATAATGG 988
Db 301 CGAGGATCTCGTGTGACCCATGCGGATGCTGCTGCCGAATATCATGTGGAATAATGG 360

QY 989 CCGCTTTTCTGGATTCATTCGACTGTGCGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 1048
Db 361 CCGCTTTTCTGGATTCATTCGACTGTGCGCGGCTGGGTGTGGCGGACCGCTATCAGGACAT 420

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